# Targeted next generation sequencing makes new molecular diagnoses and expands genotype-phenotype relationship in Ehlers-Danlos syndrome

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| **Abstract:** | Purpose:<br>Ehlers-Danlos syndrome (EDS) comprises a group of overlapping hereditary disorders of connective tissue with significant morbidity and mortality, including major vascular complications. We sought to identify the diagnostic utility of a next-generation sequencing (NGS) panel in a mixed EDS cohort.<br><br>Methods:<br>We developed and applied PCR-based NGS assays for targeted, unbiased sequencing of 12 collagen and aortopathy genes to a cohort of 177 unrelated EDS patients. Variants were scored blind to previous genetic testing and were then compared to results of previous Sanger sequencing. |

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| | Results:<br>Twenty-eight pathogenic variants in COL5A1/2, COL3A1, FBN1 and COL1A1, and four likely pathogenic variants in COL1A1, TGFBR1/2 and SMAD3 were identified by the NGS assays. These included all previously detected single nucleotide and other short pathogenic variants in these genes, and seven newly detected pathogenic or likely pathogenic variants leading to clinically significant diagnostic revisions. Twenty-two variants of uncertain significance (VUS's) were identified, seven of which were in aortopathy genes and require clinical follow-up.<br><br>Conclusion:<br>Unbiased NGS-based sequencing made new molecular diagnoses outside the expected EDS genotype-phenotype relationship and identified previously undetected clinically actionable variants in aortopathy susceptibility genes. These data may be of value in guiding future clinical pathways for genetic diagnosis in EDS. |

# Targeted next generation sequencing makes new molecular diagnoses and expands genotype-phenotype relationship in Ehlers-Danlos syndrome.

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**ABSTRACT**

**Purpose:**

Ehlers-Danlos syndrome (EDS) comprises a group of overlapping hereditary disorders of connective tissue with significant morbidity and mortality, including major vascular complications. We sought to identify the diagnostic utility of a next-generation sequencing (NGS) panel in a mixed EDS cohort.

**Methods:**

We developed and applied PCR-based NGS assays for targeted, unbiased sequencing of 12 collagen and aortopathy genes to a cohort of 177 unrelated EDS patients. Variants were scored blind to previous genetic testing and were then compared to results of previous Sanger sequencing.

**Results:**

Twenty-eight pathogenic variants in *COL5A1/2, COL3A1, FBN1* and *COL1A1*, and four likely pathogenic variants in *COL1A1, TGFBR1/2* and *SMAD3* were identified by the NGS assays. These included all previously detected single nucleotide and other short pathogenic variants in these genes, and seven newly detected pathogenic or likely pathogenic variants leading to clinically significant diagnostic revisions. Twenty-two variants of uncertain significance (VUS's) were identified, seven of which were in aortopathy genes and require clinical follow-up.

**Conclusion:**

Unbiased NGS-based sequencing made new molecular diagnoses outside the expected EDS genotype-phenotype relationship and identified previously undetected clinically actionable variants in aortopathy susceptibility genes. These data may be of value in guiding future clinical pathways for genetic diagnosis in EDS.

**Key words**

Ehlers-Danlos syndrome, High-throughput DNA sequencing, Hereditary Disorders of Connective Tissue, Aortic diseases, Collagen

## INTRODUCTION

Ehlers-Danlos syndrome (EDS) is a group of overlapping hereditary disorders of connective tissue (HDCT).[1, 2, 3] Predominant clinical phenotypes include skin fragility, easy bruising and joint hypermobility.[2] Due to generalised connective tissue fragility, blood vessels and internal organs may also be affected to a variable extent. Vascular EDS patients can present as early as the first two weeks of life with aneurysm or rupture of large blood vessels, or sudden spontaneous rupture of the bowel or other intra-abdominal organs.[2, 3, 4]

EDS is classified clinically by the 1997 Villefranche nosology.[1] The three major groups are classical, vascular and hypermobility type EDS, whilst others, including kyphoscoliosis, dermatosparaxis, arthrochalasia are extremely rare.[1, 2] The central pathological abnormality affects collagen packing or stability, mechanisms traditionally based upon certain microscopic, biochemical and genetic abnormalities in collagen types I, III, and V. Most classical EDS cases are caused by mutations in one of two genes encoding collagen type V (*COL5A1, COL5A2*); vascular EDS is largely caused by mutations in *COL3A1*, encoding collagen type III, whilst the genetics of hypermobility type EDS remains largely unresolved and is predicted to be heterogeneous.[2, 4] A number of other genes encoding extracellular matrix proteins *(PLOD1, CHST14, FKBP14; RIN2; PRDM5, ZNF469, B4GALT7, SLC39A13)* are reported as causes of additional very rare EDS presentations.[2, 4] Because of phenotypic heterogeneity and clinical overlap between EDS types, clinical evaluation alone is often not definitive and even after genetic testing, the majority of EDS cases remain without a molecular diagnosis.[1, 2]

Next generation sequencing (NGS) technologies offer the potential for genetic testing in a range of disorders including EDS.[5] Using a newly developed NGS-based panel, we screened a mixed cohort of EDS patients for variants in key collagen genes and certain other genes known to cause EDS or related connective tissue disorders. We sought to ascertain whether this approach would increase the proportion of genetic diagnoses and improve understanding of the relationship between genotype and phenotype in EDS by

comparing the results obtained by NGS with previous genetic testing of individual genes by Sanger sequencing.

## MATERIALS AND METHODS

### Selection of cases with Ehlers-Danlos syndrome

177 unrelated patients with suspected EDS referred by specialist (tertiary) clinicians to the National EDS Diagnostic Service (London, UK) were recruited to the study. The patients were predominantly female (67%) and Caucasian (89%). The mean age of the cohort was 33.6 years (range 2-78). Since the service studied complex EDS phenotypes and because of their prognostic importance, patients with vascular complications were preferentially recruited to the study. Clinical diagnoses upon first interview, based only on clinical features, were as follows: classical EDS (or overlapping syndrome) 12%, vascular EDS (or overlapping syndrome) 12%, EDS hypermobility type or benign joint hypermobility syndrome (BJHS) 43%, kyphoscoliotic EDS 2%. 7% of cases had a phenotype overlapping multiple EDS types, not falling into one specific EDS type and will be described hereafter as Complex EDS. 24% of cases had features predominantly outside the EDS spectrum, here termed "Other hereditary disorder of connective tissue (HDCT)." This term was used for patients with non-specific features of HDCT, where criteria for a specific EDS type were not adequately fulfilled and the patient did not have an arterial complication (for example osteogenesis imperfecta, myopathies). A further group not falling into a specific EDS type but with prior history of arterial complication (defined as one or more of: aortic or peripheral arterial aneurysm, dissection or rupture, cerebral aneurysm/subarachnoid haemorrhage) was designated "Other HDCT (vascular)".

Clinical categorisation was based upon 1997 Villefranche criteria[1] by specialist EDS clinicians (FMP, AV, NG – combined experience 51 years). 76 relatives were phenotyped and recruited to the study for segregation analysis. All study subjects were recruited

according to Ethics Protocol Reference 11/LO/0883 (West London Research Ethics Committee).

**Characterisation of clinical, biochemical, histological and ultrastructural phenotype**

Phenotypic data were derived from clinical notes, including diagnostic scores (according to Beighton system, Villefranche criteria, Ghent nosology and Sillence criteria),[1, 6] light and electron microscopy (LM, EM) and collagen protein analysis carried out at the National EDS Diagnostic Service, London. Genetic testing results (by conventional Sanger sequencing) in the UK National Health Service were recorded for comparison.

Skin biopsies taken from patients' upper inner arm were used for Collagen protein analysis and microscopy. Fibroblasts were cultured from skin biopsies, with collagen labelling and sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) analysis performed as described.[7] LM: Dermal tissue blocks stained with Haematoxylin & Eosin / Elastin Van Gieson, were assessed to determine changes in dermal thickness and collagen: elastin ratio. EM: skin biopsies were placed directly into 4% glutaraldehyde in 0.1M phosphate buffer and processed for routine EM as described previously.[8] Thin sections (stained with uranyl acetate and lead citrate) were examined for ultrastructural abnormalities of collagen fibril size and arrangement and appearance of fibroblast endoplasmic reticulum.

**DNA extraction and targeted exon sequencing**

Saliva samples were collected using the Oragene DNA kit (Genotek, Ontario, Canada). DNA from whole blood samples was extracted using the QIAamp DNA Blood Midi kit (Qiagen, Venlo, Netherlands). Two NGS assays were designed, to sequence the exons and exon-intron boundaries of genes commonly associated with EDS and overlapping phenotypes: (1) Collagen NGS panel: 375 primer-pairs for *COL1A1*, *COL1A2*, *COL3A1*, *COL5A1* and *COL5A2*; and (2) Aortopathy NGS panel: 363 primer-pairs for *FBN1, TGFBR1, TGFBR2, MYH11, ACTA2, SMAD3* and *MYLK* (Tables S1 & S2; Supplementary materials). Both NGS panels were used on every patient.

Multiplex PCR was performed using the Access Array (Fluidigm, South San Francisco, USA) in batches of 47 test samples and one negative control (water blank) as described.[9] Ninety-six purified samples were pooled and sequenced on the MiSeq sequencer (Illumina, San Diego, USA) generating 150bp paired-end reads.

**Read mapping, variant calling and annotation**

The quality of sequencing reads was assessed with FastQC.[10] Reads were mapped to the GRCh37/hg19 human reference sequence using BWA-MEM v0.7.2.[11] Sequence reads were realigned around insertions/deletions and base call quality scores recalibrated with GATK v2.6-5.[12] Single-nucleotide variants (SNVs) and short insertions/deletions (up to 20 nucleotides) were called with GATK UnifiedGenotyper. Variants were hard filtered to achieve minimum coverage at a variant of ≥100 reads and allele balance >0.25. Variant annotation was carried out with ANNOVAR version 2013aug23[13]. Reference transcripts of genes are shown in Table S3.

**Pathogenicity assignment**

Synonymous variants, intronic variants located outside exon/intron boundaries and SNVs with minor allele frequency > 0.1% in 1000 genomes project (phase 2 release) or the NHLBI exome sequencing project data-sets (as available in 2013Aug23 version of Annovar) were excluded from further analysis. Splice site-disrupting variants, nonsense and frameshift coding variants with allele frequency <0.1% were considered pathogenic. Substitutions of glycine residues at GlyXY repeats within collagen triple helical domains were considered pathogenic, as well as other variants previously reported as pathogenic in established variant databases (LOVD[14] and HGMD[15]) unless biochemical (collagen protein analysis), phenotype and/or segregation data suggested otherwise. Missense variants were classified according to American College of Medical Genetics and Genomics (ACMG) guidelines [16] with the special additional case of Glycine-substitutions in Collagen helical domains, which have the effect of disrupting helix formation and are therefore generally considered to be pathogenic owing to loss of function conferred by these variants. All other

variants were classified as variants of uncertain significance (VUS's) which were further categorised, based on available evidence, according to ACMG criteria.[16] Filtered variants were validated by Sanger sequencing and submitted to the LOVD database.[14] A single false positive variant was found in exon 1 of *SMAD3* (ID 382) and was removed from further analysis.

### Statistical analysis

$\chi^2$ and Fisher's exact tests were used to test for significant differences in categorical variables between individuals in different genotype or phenotype groups. The Mann-Whitney test was used to assess statistical differences between in silico prediction scores.

## RESULTS

### Clinical phenotype

Table 1 summarises the clinical phenotype spectrum tabulated by initial clinical diagnosis. There was wide phenotypic heterogeneity within each diagnostic group, with patients frequently possessing overlapping Villefranche criteria suggestive of more than one diagnostic category. Eighteen patients, distributed across diagnostic groups had marfanoid features (of which two had Ghent Marfan systemic scores ≥7). Four patients diagnosed as Other HDCT had signs consistent with osteogenesis imperfecta (OI) or an overlapping phenotype.

### Results of previous genetic testing by Sanger sequencing

The traditional route to genetic testing by Sanger sequencing is phenotype-driven, usually by sequencing one or two of the most likely causative genes, based on clinical and laboratory data.

The frequency of a detected pathogenic variant in the anticipated gene was 33% for cases initially diagnosed as classical EDS or an overlapping phenotype (7 pathogenic variants in *COL5A1/2* of 21 patients tested) although the frequency increased to 58% if those with

overlapping classical/hypermobility phenotypes were excluded. The frequency of pathogenic variants in *COL3A1* in patients initially diagnosed as vascular EDS was 50% (11 of 22 patients tested). In the 4 patients with a clinical phenotype of EDS/OI the frequency of *COL1A1/2* pathogenic variants was 75% (Table 2). Outside of the anticipated gene, further testing revealed a specific pathogenic DNA variant in only 7.8% (12/155). In addition to short variants (SNV's and short indels) in collagen genes that were considered pathogenic, a complex rearrangement was identified causing complete allelic loss of *COL3A1* & *COL5A2* (ID 444) and pathogenic variants were identified in *TNXB* (ID 67), *FBN2* (ID 1125) and *FKBP14 (homozygous,* ID 822) (Table S4). Pathogenic or likely pathogenic variants were also identified in three other patients: in *FBN1* (ID 66), *TGFBR1* (ID 706), and *SMAD3* (ID 382) (Table S4). Several incidental genetic abnormalities not considered to be contributory to EDS phenotype were also observed: a heterozygote VUS in *TNXB* (ID 79), *FLNA* variant (ID 538) and 0.1Mb polymorphic deletion identified by karyotyping (ID 801) (Table S4).

**Targeted NGS sequencing**

Amplicons of the Collagen panel achieved a mean coverage of 602x with 95.0% bases covered above 100x, whilst those of the Aortopathy panel achieved a mean coverage of 926x per amplicon with 97.4% targeted bases covered by 100 reads or more.

NGS sequence data were analysed blind to previous genetic testing. The mean number of variants called per sample was 12.7 (range 5- 25) and 28.7 (range 9-51) with the Collagen and Aortopathy NGS panels, respectively. After filtering of variants by allele frequency and variant type, a total of 28 pathogenic variants, four likely pathogenic variants and 22 VUS's were identified (Tables 3 and 4).

**Pathogenic variants identified by NGS**

In the 21 cases categorised initially as classical EDS or overlapping phenotypes, we identified pathogenic variants in nine cases (41%): seven in the *COL5A1* or *COL5A2* genes and two in *COL3A1* (Table 3). The first of these two (ID 417) had overlapping features of

classical, hypermobility and vascular EDS; the second (ID 636) had convincing clinical features entirely consistent with classical EDS (Table S5). In the 22 patients diagnosed initially as vascular EDS, 11 had pathogenic variants in *COL3A1,* whilst one with overlapping features of vascular and classical EDS had a pathogenic variant in *COL5A1* (functional corroboration was not possible as the patient declined skin biopsy - ID 1088, Table S5). One of the patients with an initial diagnosis of hypermobility type EDS (ID 824) carried a pathogenic *COL5A1* variant (Tables 3 and S5). Of the patients with an initial diagnosis of other HDCT, three had pathogenic variants in *COL1A1 (*all three diagnosed clinically with EDS/OI overlap) and a further three had pathogenic variants in *FBN1* (Table 3; Tables S5, S6). Table S7 shows the phenotype details of cases with no identified variants.

**Likely Pathogenic Variants and Variants of Uncertain Significance (VUS) identified by NGS**

Of the 26 VUS's identified, 22 were dispersed amongst either hypermobile or other HDCT patients (Table 4). These included variants in *COL1A1*, *TGFBR1, TGFBR2* and *SMAD3,* which we categorised as likely pathogenic (Tables 4 and S6). One of these patients (ID 893) carried a helical domain Arg>Cys variant in *COL1A1*, a number of which have been shown to be pathogenic in previous reports. [23]

Although two particular variants had previously been reported as pathogenic, we classified these as VUS's in our patients (Table 4 & S5): a *COL1A2* variant[17] (ID 629) due to non-segregation in first degree relatives and *COL3A1* C-propeptide variant[18] (ID 655) because of lack of clinical or biochemical corroboration in the index case or her first-degree relative who also carried the variant. Two hypermobility EDS patients were each found to have two separate VUS's: ID 38 in *COL3A1* and *COL5A2;* ID 39 in *COL1A2* and *COL3A1* (Table 4; and Table S4). One patient initially categorised clinically as classical EDS (ID 636) carried an intronic VUS in *COL5A2,* but also carried a pathogenic *COL3A1* variant (Table S4 & S5).

**In silico predictions of missense variants detected by NGS**

The majority of missense pathogenic variants detected by NGS had in silico predictive scores of, or close to 1.0 whereas the scores for VUS's were more variable and lower (mean score = 0.70, p<0.0001 for SIFT; 0.67, p=0.0005 for Polyphen2; 0.89, p=0.006 for MutationTaster; 0.60, p<0.0001 for MutationAssessor); a similar pattern was observed for predictions of evolutionary conservation (Table S8). The two variants that were previously reported as pathogenic but that we classified as VUS's (IDs 629 and 655) had high in silico prediction scores (Table S8), but lacked pathological or segregation data to support pathogenicity. In addition a helical Arg>Cys variant in *COL1A2* (ID 1151) and three other VUS's in *COL1A1, COL3A1* and *COL5A1* (IDs 39, 824, 828) also had high in silico predictions (Table S8). In the Aortopathy panel, three variants, in *SMAD3* (ID 382), *TGFBR2* (ID 814), and *TGFBR1* (ID 706) also had high in silico predictive scores: these three variants were in functionally important domains and the clinical phenotypes of these patients strongly suggested pathogenicity of the variants (Tables S6 & S8).

**Clinical, genetic and pathological correlates of collagen gene variants**

Most pathogenic DNA variants in collagen genes were associated with a corresponding collagen protein abnormality on SDS-PAGE but protein abnormalities were much less common in VUS's (81.8% vs. 11.1%; p=0.006). A similar difference in light and electron microscopy abnormalities was observed when comparing pathogenic variants with VUS (76.9% vs. 21.1%; p=0.02). There was no significant difference (p>0.05) in the frequency of presenting vascular complications between pathogenic *COL3A1* variants (38%) and those with variants of other genes or when compared with mutation-negative cases (31%) (Table S9). There was also no significant difference in Beighton score based on gene or variant-type (p>0.05).

**Comparison with Sanger sequencing**

All of the 22 short pathogenic variants in the collagen genes and the pathogenic variants in *FBN1* and *SMAD3* that were identified by previous Sanger sequencing were also identified by the NGS panels (Figure 1A). Furthermore, the NGS panels newly identified seven

pathogenic or likely pathogenic variants and 18 VUS's that had not been detected by phenotype-guided Sanger sequencing (Tables 3 & 4; Figure 1A). The Collagen NGS panel identified four unexpected pathogenic or likely pathogenic variants in genes that had not been selected for Sanger sequencing: first, a *COL3A1* variant (ID 636), in a patient previously diagnosed as classical EDS on the basis of clinical phenotype and the presence of an intronic, possible splice-disrupting *COL5A2* variant (c.1402-10T>G); second, a loss of function *COL5A1* variant in a patient with overlapping features of vascular and classical EDS phenotype (ID 1088) for whom only *COL3A1* sequencing had been undertaken; third, an Arg>Cys variant in the helical domain of *COL1A1* in a patient with a predominant hypermobility trait with fractures (ID 893) and finally a helical Glycine disrupting *COL5A1* variant in a patient with a predominant hypermobility trait (Beighton score 9/9) but minimal skin hyperextensibility (ID 824) (for details see Tables 3 and S5). In addition, six missense variants were identified with maximal or near maximal in silico prediction scores for pathogenicity (Table S8). These variants did not meet ACMG criteria for pathogenicity or likely pathogenicity and were therefore classified as VUS's. The Aortopathy NGS panel identified four new variants not previously detected by clinical or genetic investigation, in *FBN1*, *TGFBR1*, and *TGFBR2*: two were pathogenic variants of *FBN1* (IDs 766 & 378, both with initial diagnosis of "Other HDCT"), one was a likely pathogenic variant (*TGFBR2*, ID 814, with an initial clinical phenotype of hypermobility type EDS), and the fourth variant we classified as uncertain significance (*TGFBR1,* ID 475 with an initial clinical phenotype of "Other HDCT") (Table S6).

**DISCUSSION**

To our knowledge, this is the first report of the use of NGS to sequence a panel of relevant collagen and aortopathy genes in a large mixed cohort of patients with EDS or overlapping HDCT.

Our NGS panel was able to detect all previously identified short pathogenic variants in collagen and aortopathy genes and, in addition, newly identified seven pathogenic or likely

pathogenic variants in *COL1A1, COL3A1*, *COL5A1 (2 cases), TGFBR2,* and *FBN1* (2 cases), leading to new diagnoses in these patients. Of 18 newly detected VUS's, a significant proportion had partial evidence of pathogenicity, based on previous reports, clinical phenotype and in silico prediction score, including three in aortopathy genes (*TGFBR1* and *TGFBR2*) and four in *COL3A1* which, if shown to be pathogenic, alter clinical prognosis and management because of the associated high risk of arterial aneurysm, rupture and/or bowel perforation.

Pathogenic collagen variants did not always correlate with the expected phenotype. In two patients we found pathogenic *COL3A1* variants associated with a clinical phenotype of classical or overlapping classical EDS, one of whom (ID 636) also had an intronic *COL5A2* variant, possibly splice site disrupting, which could also contribute to his phenotype. Classical EDS is usually associated with pathogenic variants in *COL5A1/2*, but has rarely been associated with those in *TNXB*, *COL1A1* or *COL3A1*.[19, 20] Pathogenic *COL3A1* variants are normally considered diagnostic of vascular EDS, with reduced life expectancy from arterial and bowel complications. [4,21]

Since previous vascular EDS series have been mostly selected by clinical criteria (Villefranche) along with collagen type III protein deficiency or pathogenic *COL3A1* variants, the frequency of other connective tissue gene variants in clinical vascular EDS phenotypes is unknown.[4, 21] One of our patients clinically classified as having features predominantly of vascular EDS (ID 1088) showed a Leu1055X variant of *COL5A1*. One pedigree with a pathogenic *COL5A1* variant segregating with a vascular EDS phenotype including arterial ruptures has been recently reported (LOVD ID AN004203).[14,22] A further patient (ID 824) for whom a pathogenic *COL5A1* variant was found, had an initial diagnosis of Hypermobility type EDS on account of extensive hypermobility, soft but not hyper-extensible skin and family history of sudden cardiac death in a second degree relative; functional corroboration was not possible for this patient as they were lost to follow-up. As far as we are aware such a phenotypic pattern has not been observed with a pathogenic *COL5A1* variant, probably

because *COL5A1* sequencing to date has mostly been carried out in phenotypically classical cases.[2,3,19]

Nine VUS's with high in silico prediction scores or other evidence for pathogenicity were observed. These included one Arg>Cys variant within the helical domain of *COL1A2* (ID 1151, p.Arg1338Cys) (Tables S4 & S5). Arg>Cys variants at helical locations in *COL1A1* have been reported previously as predisposing to arterial fragility and other phenotypes (Table S5).[23] Although the *COL1A2* variant may be pathogenic, little evidence exists at the present time to establish its pathogenicity.

We also observed four variants in aortopathy genes *TGFBR1, TGFBR2, SMAD3* for which there was moderate or supporting evidence of pathogenicity (Table S6). Three of these were considered to be likely pathogenic: two in the functionally active kinase domains of *TGFBR1* (ID 706) and *TGFBR2* (ID 814) known to be associated with the majority of Loeys-Dietz syndrome variants to date,[24] and the third adjacent to the MH2 domain of *SMAD3* (ID 382), which is known to regulate TGF-beta signalling.[25] Coronary artery dissection (seen in our patient) and other vascular complications have previously been caused by *SMAD3* variants.[26] The fourth variant, in *TGFBR1* (ID 475) was in a patient with Other HDCT, bone fragility and a systolic murmur (and normal *COL1A1/2*). This variant was reported previously as a VUS associated with bicuspid aortic valve,[27] and bone fragility is a recent addition to the LDS clinical spectrum,[28] so this variant may underlie some of our patient's features but the evidence is less clear.

We re-classified two variants with high in silico prediction scores as VUS's, though previously reported as pathogenic: The *COL1A2* Arg708Glu variant detected in ID 629 was reported previously in a Marfanoid patient, [17] but segregation analysis revealed hypermobility in all of the patient's seven offspring, hypermobility in her (unrelated) husband, multiple fractures in one of the two offspring who carried the variant and no fractures in the remaining five offspring, leading us to classify this variant as a VUS. The *COL3A1*

p.Lys1313Arg variant detected in ID 655 has been previously reported in two unrelated patients with vascular EDS.[18] However, collagen microscopy and biochemistry were normal in the patient, neither the patient nor her sister, who also carried the variant, had features of vascular EDS and structural studies indicated that the variant was unlikely to impair C-propeptide-mediated helical winding.[29,30]

Consistent with previous reports, we observed significant phenotypic overlap between our EDS diagnostic categories and other HDCT as well as overlap amongst patients with pathogenic variants in individual causative genes.[2,3,6,19,20,22,23] These factors point to the limitations of phenotype-driven genetic testing of individual candidate genes. The NGS approach presented here permits wider genetic testing than is possible with traditional Sanger sequencing, allowing more comprehensive genetic diagnosis. This led to new and revised diagnoses of patients in our cohort and widened the phenotypic spectrum ascribed to individual genes.

Based on our previous experience and taking the results from this study as a whole, some general recommendations can be made. For cases with phenotypes overlapping classical or vascular EDS, the yield of pathogenic variants is high in the normally associated gene (*COL3A1*, *COL5A1*, *COL5A2*) and occasionally one may identify pathogenic variants in another fibrillar collagen gene. Cases of uncomplicated EDS-Hypermobility type with no family history of vascular complication had a low yield of pathogenic variants and a large number of VUS's (most of which will not be fed back): NGS panel testing for such cases is unlikely to be diagnostic. Conversely, potential connective tissue cases with a history of vascular complication, marfanoid features, or with a significant family history should undergo NGS panel testing for collagen and aortopathy genes, as our results indicate a reasonable likelihood of identifying pathogenic variants in one of these genes. Similarly, cases of EDS or other HDCT overlapping with osteogenesis imperfecta should also undergo collagen gene testing to exclude pathogenic *COL1A1* or *COL1A2* variants.

The interpretation of missense variants includes correlation with the complete clinical phenotype. In keeping with ACMG guidelines, we classify variants that are supported by some evidence of pathogenicity (e.g. high in silico scores and presence in functionally active domains) or associated with clinical features such as aortopathy as “likely pathogenic” and recommend they are followed up clinically with vascular imaging, familial segregation studies and available structural or biochemical studies including EM or protein analysis. Initial genetic counseling for such patients should include the fact that the true significance of the variant will not be known until these additional tests are complete. Although in the short term some of these VUS’s may add some uncertainty to the diagnostic process, we believe this is greatly outweighed by the prospect of making specific genetic diagnoses, which would otherwise go undetected and form the basis for preventative screening in relatives. In the longer term, assignment of pathogenicity is likely to be facilitated by data from ongoing large-scale genome sequencing projects in patient and control cohorts.

We used the PCR-based Fluidigm Access Array followed by Illumina MiSeq. Mean coverage per amplicon was greater than 140x for all amplicons, comparable to previously reported assays using this methodology.[9,31] Although this method is unable to detect large deletions or chromosomal rearrangements, these are rare in EDS.[2] In addition, whilst false positive variant calls have been previously reported with this approach,[31] we detected only a single variant (in exon 1 of *SMAD3*) that could not be confirmed by Sanger sequencing. Since NGS methods have higher throughput, achieve greater coverage and may be more cost-efficient than conventional Sanger sequencing,[31] they may be applicable to wider phenotypic groups, for which this study may serve as a guide to future genetic testing. We suggest that the higher throughput, lower cost, and comparable or increased diagnostic yield of NGS could alter the optimal diagnostic pathway, such that genetic testing with NGS panels can occur earlier in the diagnostic pathway, prior to tertiary or quaternary clinical appraisal (Figure 1B).

## SUPPLEMENTARY DATA

Supplementary information is available at the *Genetics in Medicine* website.


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## DISCLOSURE

TJA has received speaker honoraria and has research collaborations with Illumina and consultancy fees from AstraZeneca. Other authors have no disclosures.

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## FIGURE LEGENDS

**Figure 1. A.** Yield of rare variants using traditional Sanger method (left) compared with the NGS panel (right). **B.** Potential alternative clinical pathway to genetic diagnosis in EDS. Boxed numbers show the number of rare pathogenic variants and VUS's identified in each group; percentages are the proportion of new pathogenic or likely pathogenic rare variants in our cohort of 177 EDS referrals. "Other" genetic abnormalities are those that were thought to underlie the EDS phenotype but are not covered by the NGS panel (3 pathogenic variants in *TNXB*, *FBN2*, *FKBP14* & 1 large copy number variant; 1 VUS, a TNXB gene duplication). Dashed arrow indicates the potential for NGS panel to become accessible to clinicians in secondary care.

Figure

Click here to download Figure Figure1_BW.gif

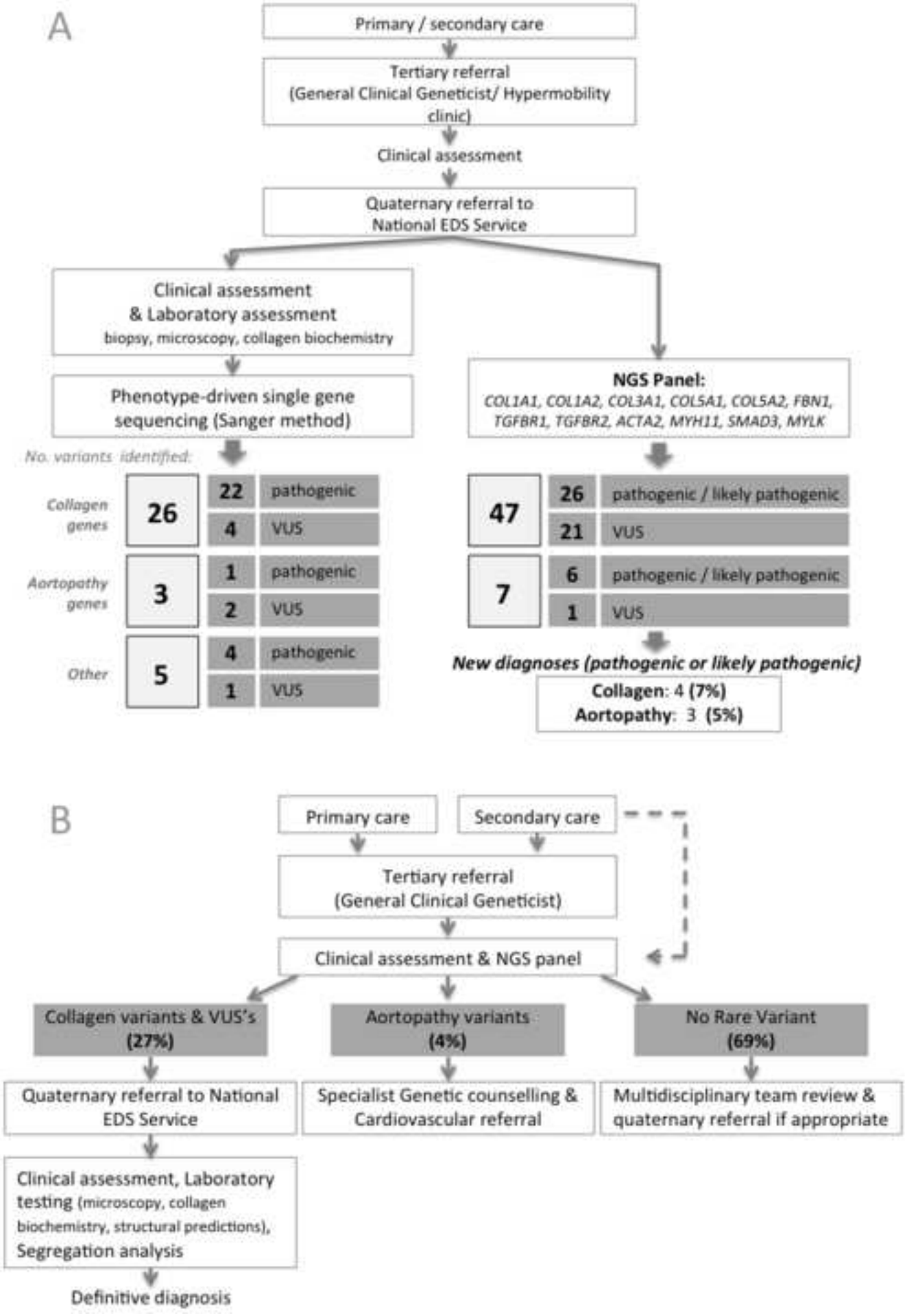

**Table 1** Clinical spectrum of cohort

| Initial Clinical Diagnosis [a] | No. of cases | Mean Age (range) | Mean Beighton score | No. (%) meeting Villefranche EDS criteria [c] | | | | Arterial complication [d] |
|---|---|---|---|---|---|---|---|---|
| | | | | Classical | Vascular | Hypermobility | KPS | |
| **Classical** [a] | 21 | 34.8 (19-78) | 7.3 | 21 (100%) | 3 (14%) | 15 (71%) | 0 | 2 (10%) |
| **Vascular** [a] | 22 | 30.7 (6-48) | 4.8 | 5 (23%) | 21 (95%) | 10 (45%) | 0 | 11 (50%) [e] |
| **Hypermobility** | 76 | 32.7 (2-67) | 5.8 | 21 (28%) | 14 (18%) | 73 (96%) | 8 (11%) | 14 (20%) |
| **Rare & Complex EDS** [b] | 16 | 22 (2-55) | 6.2 | 7 (44%) | 4 (25%) | 7 (44%) | 6 (38%) | 0 |
| **Other HDCT** | 11 | 32.6 (4-52) | 6.0 | 5 (45%) | 1 (9%) | 8 (73%) | 3 (27%) | 0 |
| **Other HDCT (vascular)** | 31 | 43.4 (8-72) | 4.5 | 11 (35%) | 18 (58%) | 22 (71%) | 1 (3%) | 31 (100%) |

EDS, Ehlers-Danlos syndrome; KPS, kyphoscoliosis type of EDS; HDCT, hereditary disorder of connective tissue (phenotypes further elaborated in Supplementary Table 3).

**a**. Initial Clinical Diagnosis refers to most applicable classification at first specialist EDS consultation: Classical cases included 9 cases of classical/hypermobility type overlap, Vascular cases included 3 vascular/hypermobile and 2 vascular/classical overlap. **b.** Rare EDS refers to EDS types outside classical, vascular and hypermobility types. **c.** Villefranche classification: numbers (percentages) indicate the number (percent) of patients in each group meeting at least one major criterion for each EDS type. **d.** Arterial complication: history of one or more of aortic or peripheral arterial aneurysm, dissection or rupture, cerebral aneurysm / subarachnoid haemorrhage at first EDS consultation. **e.** $p = 0.002$ (vascular vs. other EDS).

**Table 2** Previously identified genetic and pathological abnormalities

| Initial Clinical Diagnosis [a] | No. of cases | Gene affected [b] | | | | Collagen abnormality [c] | LM/EM abnormality |
|---|---|---|---|---|---|---|---|
| | | *COL1A1* *COL1A2* | *COL3A1* | *COL5A1* *COL5A2* | Other | | |
| **Classical** | 21 | 0/3 | 1/7 | 7/11 | 1/2 | 1/9 (11%) | 11/15 (73%) [d] |
| **Vascular** | 22 | 0/1 | 11/17 | 0/1 | 2/8 | 7/11 (64%) | 9/13 (69%) |
| **Hypermobility** | 76 | 0/6 | 0/24 | 0/11 | 0/5 | 0/21 | 6/22 (27%) |
| **Rare & Complex EDS** | 16 | 0/2 | 0/6 | 0/3 | 1/1 | 0/1 | 3/7 (43%) |
| **Other HDCT** | 11 | 3/6 | 0/1 | 0/0 | 0/2 | 3/5 (60%) [e] | 5/6 (83%) |
| **Other HDCT (vascular)** | 31 | 0/4 | 0/23 | 0/5 | 3/16 | 3/9 (33%) [f] | 9/18 (50%) |

LM, light microscopy. EM, electron microscopy. HDCT, hereditary disorder of connective tissue.

**a.** Initial Clinical Diagnosis refers to most applicable classification at first specialist EDS consultation (as in Table 1). **b.** Pathogenic variants identified by Sanger sequencing (numerator, number of pathogenic variants; denominator, number of separate genetic tests carried out in each category. **c.** Abnormality of the corresponding collagen type on SDS-PAGE. **d.** Four of these cases had collagen rosettes on EM. **e.** These three patients had abnormalities of collagen I had phenotypes overlapping with osteogenesis imperfecta; two had pathogenic variants in *COL1A1/COL1A2*. **f.** Two of these three cases had collagen III deficiency; the third case had collagen I deficiency; none had rare variants in the corresponding genes.

**Table 3** Pathogenic variants identified by the Collagen and Aortopathy NGS panels

| Initial Clinical Diagnosis [a] | ID | Gene affected | Variant | Functional category | Novel/reported: phenotype | Sanger detected [b] |
|---|---|---|---|---|---|---|
| Classical | 636 | *COL3A1* | c.2329G>C: p.Gly777Arg | Missense | Novel | N |
| Classical | 417 | *COL3A1* | c.1922_1923+2delAAGT | Splice site | Reported: vascular EDS [c] | Y |
| Classical | 582 | *COL5A1* | c. 2034+1G>T | Splice site | Novel | Y |
| Classical | 31 | *COL5A1* | c.2903delC: p.Pro968LeufsX106 | Frameshift | Novel | Y |
| Classical | 429 | *COL5A1* | c.757C>T: p.Gln253X | Stop gain | Novel | Y |
| Classical | 581 | *COL5A1* | c.4552C>T: p.Gln1518X | Stop gain | Reported: Classical EDS [d] | Y |
| Classical | 627 | *COL5A1* | c.831C>A: p.Tyr277X | Stop gain | Novel | Y |
| Classical | 1129 | *COL5A1* | c.1670dupT: p.Leu557fsX? | Frameshift | Novel | Y |
| Classical | 62 | *COL5A2* | c.3445G>T: p.Gly1149Cys | Missense GlyXY | Novel | Y |
| Vascular | 448 | *COL3A1* | c.4319C>T: p.Pro1440Leu | Missense | Reported: Vascular EDS [e] | Y |
| Vascular | 765 | *COL3A1* | c.1662+1G>A | Splice site | Reported: Vascular EDS [d] | Y |
| Vascular | 37 | *COL3A1* | c.2564G>A: p.Gly855Asp | Missense GlyXY | Reported: Vascular EDS [d] | Y |
| Vascular | 42 | *COL3A1* | c.2417C>T: p.Pro806Leu | Missense | Novel | Y |
| Vascular | 46 | *COL3A1* | c.1771G>C: p.Gly591Arg | Missense GlyXY | Novel | Y |
| Vascular | 76 | *COL3A1* | c.2771G>A: p.Gly924Asp | Missense GlyXY | Reported: Vascular EDS [d] | Y |
| Vascular | 405 | *COL3A1* | c.1662+1G>A | Splice site | Reported: Vascular EDS [d] | Y |
| Vascular | 483 | *COL3A1* | c.2553+1G>A | Splice site | Reported: Vascular EDS [d] | Y |
| Vascular | 733 | *COL3A1* | c.2816G>A: p.Gly939Asp | Missense GlyXY | Reported: Vascular EDS [d] | Y |
| Vascular | 420 | *COL3A1* | c.1150-2A>T | Splice site | Novel | Y |
| Vascular | 443 | *COL3A1* | c.3525+1G>A | Splice site | Novel | Y |
| Vascular | 1088 | *COL5A1* | c.3164T>A: p.Leu1055X | Stop gain | Novel | N |
| Hypermobility | 824 | *COL5A1* | c.4564G>T: p.Gly1522Cys | Missense | Novel | N |
| Other HDCT (OI/EDS) | 527 | *COL1A1* | c.1265delG: p.Gly422AlafsX119 | Frameshift | Novel | Y |
| Other HDCT (OI/EDS) | 36 | *COL1A1* | c.643G>A: p.Gly215Ser | Missense GlyXY | Reported: OI/OI-EDS [g] | Y |
| Other HDCT (OI/EDS) | 559 | *COL1A1* | c.662G>C: p.Gly221Ala | Missense GlyXY | Novel | Y |
| Other HDCT (vascular) | 66 | *FBN1* | c.3781T>A: p.Tyr1261Asn | Missense | Reported: Marfan [f] | Y |
| Other HDCT (vascular) | 378 | *FBN1* | c.1775G>A: p.Gly592Asp | Missense | Reported: Marfan [h] | N |
| Other HDCT (vascular) | 766 | *FBN1* | c.3373C>T: p.Arg1125X | Stop gain | Reported: Marfan [i] | N |

EDS, Ehlers-Danlos syndrome; HDCT, hereditary disorder of connective tissue (phenotypes further elaborated in Table S4); OI, osteogenesis imperfecta. Missense GlyXY, substitution of a Gly residue in the helical domain of the corresponding collagen subtype.

**a.** Initial Clinical Diagnosis refers to most applicable EDS type at first specialist EDS consultation (though some cases overlap multiple EDS types); **b.** variants detected (Y) or not detected (N) by previous clinical diagnostic testing (Sanger method); **c.** c.1923+2_+5delTAAG reported pathogenic in LOVD; **d.** LOVD; **e.** Pro1440Ser reported as pathogenic in LOVD (Morissette et al., 2014) and Pro1440Leu pathogenicity supported by structural prediction (Vandersteen, unpublished); **f.** Y1261C (HGMD CM990591), Y1261D (HGMD CM547000); **g.** Vandersteen et al., 2013 **h.** HGMD CM013919 **i.** HGMD CM055245

**Table 4** Variants of Uncertain Clinical Significance and Likely Pathogenic variants identified in the Collagen and Aortopathy NGS panels

| Initial Clinical Diagnosis | ID | Gene affected | Variant | Functional category | Novel/reported: phenotype | Sanger detected |
|---|---|---|---|---|---|---|
| Classical | 49 | *COL3A1* | c.3511G>A: p.Glu1171Lys | Missense | Novel | N |
| Classical | 636 | *COL5A2* | c.1402-10T>G | Intronic [a] | Novel | Y |
| Vascular | 444 | *COL1A1* | c.3755G>A: p.Arg1252His | Missense | Novel | N |
| Vascular | 384 | *COL1A1* | c.3466A>G: p.Asn1156Asp | Missense | Novel | Y |
| Hypermobility | 893 | *COL1A1* | c.2980C>T: p.Arg994Cys | Missense | Novel [d] | N |
| Hypermobility | 478 | *COL1A1* | c.4315A>G: p.Ile1439Val | Missense | Novel | N |
| Hypermobility | 828 | *COL1A1* | c.3301G>A: p.Glu1101Lys | Missense | Novel | N |
| Hypermobility | 39 | *COL1A2* | c.2861T>C: p.Ile954Thr | Missense | Novel | N |
| Hypermobility | 558 | *COL1A2* | c.1159G>C: p.Ala387Pro | Missense | Novel | N |
| Hypermobility | 1151 | *COL1A2* | c.4012C>T: p.Arg1338Cys | Missense | Novel | N |
| Hypermobility | 38 | *COL3A1* | c.198A>G: p.Ile66Met | Missense | Novel | N |
| Hypermobility | 39 | *COL3A1* | c.2044G>A: p.Glu682Lys | Missense | Novel | N |
| Hypermobility | 655 | *COL3A1* | c.3938A>G: p.Lys1313Arg | Missense | Reported: Vascular EDS [b] | Y |
| Hypermobility | 34 | *COL5A1* | c.4068G>A: p.Ala1356Ala | Predicted splice site disruption | Novel | N |
| Hypermobility | 66 | *COL5A1* | c.805G>A: p.Glu269Lys | Missense | Novel | N |
| Hypermobility | 734 | *COL5A1* | c.3257C>T: p.Ala1086Val | Missense | Novel | N |
| Hypermobility | 799 | *COL5A1* | c.2497C>T: p.Pro833Ser | Missense | Novel | N |
| Hypermobility | 38 | *COL5A2* | c.2228A>C: p.Lys743Thr | Missense | Novel | N |
| Hypermobility | 671 | *COL5A2* | c.470C>T: p.Pro157Leu | Missense | Novel | N |
| Hypermobility | 814 | *TGFBR2* | c.1538T>C: p.Val513Ala | Missense | Novel [d] | N |
| Other HDCT | 475 | *TGFBR1* | c.214A>G: p.Ile72Leu | Missense | Novel | N |
| Other HDCT | 804 | *COL1A1* | c.584C>T: p.Ala195Val | Missense | Novel | N |
| Other HDCT | 629 | *COL1A2* | c.2123G>A: p.Arg708Gl | Missense | Reported: Marfanoid [c] | Y |
| Other HDCT | 708 | *COL3A1* | c.2002C>A: p.Pro668Thr | Missense | Novel | N |
| Other HDCT (vascular) | 382 | *SMAD3* | c.1218G>C: p.Trp406Cys | Missense | Novel [d] | Y |
| Other HDCT (vascular) | 706 | *TGFBR1* | c.827T>C:p.Leu276Pro | Missense | Novel [d] | Y |

Column headings and abbreviations as for Table 3. **a.** possible splice site disruption, but this patient also carries a pathogenic *COL3A1* variant and his definitive diagnosis was altered to vascular EDS. **b.** LOVD; ExAC database: likely benign variant (freq. 1:500) **c.** HGMD CM900074; DBSNP rs72658163. **b. & c.** both these variants have been previously reported as pathogenic but are classified here as VUS (see text). **d**. variants classified as Likely Pathogenic; see also Tables S5 and S6.

**Table S1** Oligonucleotide sequences of Collagen NGS panel

| Gene | Assay_Name | Forward Primer | Reverse Primer | Length | % GC | Amplicon | Chr | From | To |
|---|---|---|---|---|---|---|---|---|---|
| COL1A1 | COL1A1_1 | AAGTCCATGTGAAATTGTCTCCC | CCCCCTTGGACGTTGGTG | 194 | 52 | AAGTCCATGTGAAATTGTCTCCCATTTTTTGGCTTTTGI | chr17 | 48262737 | 48262930 |
| COL1A1 | COL1A1_10 | CACATATGGGCATGGGGAC | GACACCACCCTCAAGAGCC | 190 | 62 | CACATATGGGCATGGGGACCCTGGCATGGCAGGAGT | chr17 | 48263932 | 48264121 |
| COL1A1 | COL1A1_11 | GCGGGCGGGGTTCTTG | CCCAGCCACCTCAAGAGAAG | 167 | 60 | GCGGGCGGGGTTCTTGCGGSTKCCCTCTGGGCTCCGC | chr17 | 48264044 | 48264210 |
| COL1A1 | COL1A1_12 | GTCACGGTCACGAACCACATT | TAATCCCCACTCTCTTCCCTCTC | 183 | 54 | GTCACGGTCACGAACCACATTGGNNNNMNYNNYCC( | chr17 | 48264131 | 48264313 |
| COL1A1 | COL1A1_13 | CCATGAGCAGAGGGGATGAG | TTTCTCAAACCATTTCCCCCACT | 166 | 53 | CCATGAGCAGAGGGGATGAGGKGCTAYATAYAAYAG | chr17 | 48264345 | 48264510 |
| COL1A1 | COL1A1_14 | TGTCCCTGAACCCTTCTCCAG | GGCCTGAACTGCCTTTTTTATCT | 198 | 57 | TGTCCCTGAACCCTTCTCCAGAGAGRCAAAGGGTGCC | chr17 | 48264733 | 48264930 |
| COL1A1 | COL1A1_15 | CTCCTATCCCACAGCACAGCAT | CCTGACAGTTTGTCCCTTTCTCT | 190 | 56 | CTCCTATCCCACAGCACAGCATGGRGACTGGGGAGG( | chr17 | 48265185 | 48265374 |
| COL1A1 | COL1A1_16 | CCTAGAAGAGAGAAAGGGACAAACT | AAGAGCTCATGCTTTCCTTGC | 197 | 56 | CCTAGAAGAGAGAAAGGGACAAACTGTCAGGCRGAA | chr17 | 48265344 | 48265540 |
| COL1A1 | COL1A1_17 | ACCAGGTACAGGGAACTGGAG | CCCCATCCTGGCCCTT | 198 | 51 | ACCAGGTACAGGGAACTGGAGCCCAGCTAYTTACAG1 | chr17 | 48265857 | 48266054 |
| COL1A1 | COL1A1_18 | GCAGGGAAGCAGCAGACA | CCAGTACCCTCAGCATGGC | 187 | 57 | GCAGGGAAGCAGCAGACAAGGCTGTGGTCATGGAG1 | chr17 | 48266054 | 48266240 |
| COL1A1 | COL1A1_19 | GCTGAGGGTACTGGCATGG | CTCTGGCCTGACTCTTTCTTCTC | 174 | 58 | GCTGAGGGTACTGGCATGGGGGCTGGGGACTGCTYA | chr17 | 48266227 | 48266400 |
| COL1A1 | COL1A1_2 | TGGGGGGAAAGTTGGTTGG | AGAGTCACACCGGAGCC | 200 | 55 | TGGGGGGAAAGTTGGTTGGRTGGGAGGGAGCYAGG | chr17 | 48262812 | 48263011 |
| COL1A1 | COL1A1_20 | TCCTGTGATGGTTTTTCTCAGGG | CCTCACCCCTGTTTGCCTC | 182 | 58 | TCCTGTGATGGTTTTTCTCAGGGMCCCCCAAGGTGAC | chr17 | 48266480 | 48266661 |
| COL1A1 | COL1A1_21 | CTCCCCAGCTCTGCACAC | CTGGTCCTGCTGGCAAAGAAG | 189 | 58 | CTCCCCAGCTCTGCACACCTCCGGAGCTGCAGAGATC | chr17 | 48266686 | 48266874 |
| COL1A1 | COL1A1_22 | ATCAGCACCAGGGGATCCTTTC | GAGTCTGACAGCCCCTCCTATC | 184 | 57 | ATCAGCACCAGGGGATCCTTTCTCGCCAGCAGGGCNI | chr17 | 48266747 | 48266930 |
| COL1A1 | COL1A1_23 | ATCATTGGGTCCTCAGTCAGC | GATGAGTTGGCTGTTCTCCCTC | 197 | 56 | ATCATTGGGTCCTCAGTCAGCCCCACCATCCTTCTGGC | chr17 | 48266947 | 48267143 |
| COL1A1 | COL1A1_24 | GAGGGAGAACAGCCAACTCATC | GGACGGGTCCAGGCTT | 191 | 60 | GAGGGAGAACAGCCAACTCATCCGACCCAGCTGCCC1 | chr17 | 48267122 | 48267312 |
| COL1A1 | COL1A1_25 | GGGCACAGAGGGCCAAG | CTCCCCCAGGTAGTGGAAACTC | 197 | 60 | GGGCACAGAGGGCCAAGCCAYTCACAATGGGGYCAG | chr17 | 48267337 | 48267533 |
| COL1A1 | COL1A1_26 | CTCCCCTGAGGATGGCTGAC | GCATCTCTCCAATCTGACTCCTT | 183 | 56 | CTCCCCTGAGGATGGCTGACRCCTTTGTCCTCATTCCR | chr17 | 48267591 | 48267773 |
| COL1A1 | COL1A1_27 | TGCTGTGTGAAGGGAGGGAA | GCTCTCCTGGGGTCATCTACT | 186 | 59 | TGCTGTGTGAAGGGAGGGAAGGGCCAAGTATGGGG | chr17 | 48267845 | 48268030 |
| COL1A1 | COL1A1_28 | CTATGTGTTAGGGCAGAAGGTGG | CTTGCCCCACACTGGAAATCT | 190 | 54 | CTATGTGTTAGGGCAGAAGGTGGGGAGGCGGCCACC | chr17 | 48268138 | 48268327 |
| COL1A1 | COL1A1_29 | AGAGATGGGAGCCATGTAGGG | CCTCACTCCAGTCTTCTTGGTTG | 188 | 55 | AGAGATGGGAGCCATGTAGGGCTCAGGGGAGGGGG | chr17 | 48268695 | 48268882 |
| COL1A1 | COL1A1_3 | GGGGCACCAACGTCCAAG | ATAGTGCCCTCTCTCCATCACTC | 167 | 59 | GGGGCACCAACGTCCAAGGGGGCCACATMGATGAT( | chr17 | 48262909 | 48263075 |
| COL1A1 | COL1A1_30 | GCAGGAGGGGTGAGACCTG | CCTTCACATGCCCTGTCCTT | 190 | 60 | GCAGGAGGGGTGAGACCTGGTCCCTGGGCCACTTGC | chr17 | 48269087 | 48269276 |
| COL1A1 | COL1A1_31 | CTCTCGCCCTAGAAGGGAAGG | TTTTGCTCACTGTCTGTTCCTCT | 184 | 58 | CTCTCGCCCTAGAAGGGAAGGACAGGGCATGTGAAG | chr17 | 48269240 | 48269423 |
| COL1A1 | COL1A1_32 | cctctagttgATGGCTGTCTGATT | TAAACCTTCCCTCCCTTCTTCCC | 190 | 57 | cctctagttgATGGCTGTCTGATTAGCTAGGAGCGGGGG | chr17 | 48269740 | 48269929 |
| COL1A1 | COL1A1_33 | GACCAAAGAGGTGTTTCCTACCC | GAGATCTGGGGAGCAGAAAAGG | 198 | 59 | GACCAAAGAGGTGTTTCCTACCCCTACCTCCCAGCAT( | chr17 | 48269942 | 48270139 |
| COL1A1 | COL1A1_34 | GCACAGAGAGAACACTACAGTCA | CTCCTAACCCTGAGTTCCCCTT | 193 | 58 | GCACAGAGAGAACACTACAGTCACGGGGAGGCCGAC | chr17 | 48270057 | 48270249 |
| COL1A1 | COL1A1_35 | GCCTCTAGCACCCCTCCT | CCTCAACCCTAACTCCCTTTCTC | 164 | 56 | GCCTCTAGCACCCCTCCTGCAGGGAGGAGAAAGTGC( | chr17 | 48270273 | 48270436 |
| COL1A1 | COL1A1_36 | tgGCTCTTCATGGATCCTCACTT | TTGTCCTGTCTGCCTCCCT | 188 | 57 | tgGCTCTTCATGGATCCTCACTTAATASTCACAGCRGC/ | chr17 | 48271272 | 48271459 |
| COL1A1 | COL1A1_37 | AAGGATGGGAGGCACGAAAG | CTTCTCCCCAAGTCCCACTCATA | 180 | 58 | AAGGATGGGAGGCACGAAAGCAGCAGTGRGGACAG | chr17 | 48271405 | 48271584 |
| COL1A1 | COL1A1_38 | GGCCAAGCCAGGCTGAAAG | GAGCCACAAACTTGAGACCCTAA | 180 | 59 | GGCCAAGCCAGGCTGAAAGCCTGGGGCCTCAYCTTG( | chr17 | 48271678 | 48271857 |
| COL1A1 | COL1A1_39 | GTCTCAAGTTTGTGGCTCTTTGC | GAGTTCACTGGCCTCCTCTCC | 177 | 60 | GTCTCAAGTTTGTGGCTCTTTGCCACGGGCCAAAAGA | chr17 | 48271840 | 48272016 |
| COL1A1 | COL1A1_4 | AGTGATGGAGAGAGGGCACTATG | CAGACTGGCAACCTCAAGAAGG | 196 | 62 | AGTGATGGAGAGAGGGCACTATGGCCTGGCCAAAAV | chr17 | 48263054 | 48263249 |
| COL1A1 | COL1A1_40 | CCAGGCAATGAGGGTGGA | GATGGCCCCTCACCACA | 200 | 63 | CCAGGCAATGAGGGTGGAGYGRGAKGGGGCRGGCA( | chr17 | 48272036 | 48272235 |
| COL1A1 | COL1A1_41 | GGCTCCTCTTCCTTTCTGGATTT | CGACTCTCAGCTCATCCTCTTCT | 174 | 58 | GGCTCCTCTTCCTTTCTGGATTTCCCTCAGGGGGCTCC | chr17 | 48272323 | 48272496 |

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|---|---|---|---|---|---|---|---|---|---|
| COL1A1 | COL1A1_42 | CCAGTGCATGGGGTGGG | CCCCTTTCCCTCTGCTCCTA | 191 | 60 | CCAGTGCATGGGGTGGGCAGAAGGGAGAGTTTGGTA | chr17 | 48272552 | 48272742 |
| COL1A1 | COL1A1_43 | CCTAGGAGCAGAGGGAAAGGG | GCCACTTTCTAACCTCAGAGTCC | 178 | 54 | CCTAGGAGCAGAGGGAAAGGGGCAGGCAGGCTGCA | chr17 | 48272721 | 48272898 |
| COL1A1 | COL1A1_44 | TGAGGTTAGAAAGTGGCAAAGGG | GTTTCCCAGGGTGGCTTCTGATA | 188 | 55 | TGAGGTTAGAAAGTGGCAAAGGGGACACTGAGTCGC | chr17 | 48272882 | 48273069 |
| COL1A1 | COL1A1_45 | CACTCTGGGTCCCTTTGGTTTG | TCTCTTCCTTCTCGCTGACATCT | 181 | 57 | CACTCTGGGTCCCTTTGGTTTGGGGAACAGGGAGACA | chr17 | 48273195 | 48273375 |
| COL1A1 | COL1A1_46 | CCCATTGTCAGCCCCAAGAG | CAGTGCTCAGTGGACTTAACGG | 164 | 58 | CCCATTGTCAGCCCCAAGAGCAGAYACTGAGACCCCT | chr17 | 48273440 | 48273603 |
| COL1A1 | COL1A1_47 | GGCCAGTCCCTAGAGTTCCT | GCTGTCTCCCATCTCATCTGACT | 169 | 60 | GGCCAGTCCCTAGAGTTCCTGGGGAGCCCYTTCCAGA | chr17 | 48273603 | 48273771 |
| COL1A1 | COL1A1_48 | AGAAGTCAGATGAGATGGGAGACA | CCAGAGTCCCACCATGAATGAAT | 195 | 53 | AGAAGTCAGATGAGATGGGAGACAGCCTTGTTCCCCC | chr17 | 48273746 | 48273940 |
| COL1A1 | COL1A1_49 | ATTCATTCATGGTGGGACTCTGG | AGGCTCTTTCTCAGATCTAGGTG | 198 | 47 | ATTCATTCATGGTGGGACTCTGGGGATGTGGAGGACC | chr17 | 48273918 | 48274115 |
| COL1A1 | COL1A1_5 | GACAGTGACGCTGTAGGTGAAG | TTCCTGCGCCTGATGTCCA | 177 | 59 | GACAGTGACGCTGTAGGTGAAGCGGCTGKTGCCCTC | chr17 | 48263151 | 48263327 |
| COL1A1 | COL1A1_50 | GGACTTGGGGAGCTTAAATGACT | ACTTGGGCTTCATTTAGGAGCTG | 169 | 46 | GGACTTGGGGAGCTTAAATGACTCAAAGGTGASNNA | chr17 | 48274334 | 48274502 |
| COL1A1 | COL1A1_51 | GACAAGGAAGGGCCATTAGAACA | GGCATGATGGTCTTTTCTCTCCC | 181 | 55 | GACAAGGAAGGGCCATTAGAACACATCACTGTGGACC | chr17 | 48274443 | 48274623 |
| COL1A1 | COL1A1_52 | CAAATGTGGTGGAGTGGAAATTG | CCCAGCCTTCCCCTTCTTTTTT | 198 | 48 | CAAATGTGGTGGAGTGGAAATTGCAGGACYCAACCC | chr17 | 48275010 | 48275207 |
| COL1A1 | COL1A1_53 | TCTATAGGAGAGTCTGTGTGTTTGT | GAAGGTTGACAGGGACTTGTCTT | 164 | 45 | TCTATAGGAGAGTCTGTGTGTTTGTAGAAGGAGTRTG | chr17 | 48275251 | 48275414 |
| COL1A1 | COL1A1_54 | TCTTCCCTCCAAAAGACCAAAGC | TCCCAACAGGCATGAATGACTAC | 184 | 53 | TCTTCCCTCCAAAAGACCAAAGCCCRAGGAGGCATAT | chr17 | 48275464 | 48275647 |
| COL1A1 | COL1A1_55 | TCCTCTGGATACCCATTCTCTC | CCGTCTTCTGCCTTTCAATTCAC | 182 | 49 | TCCTCTGGATACCCATTCTCTCTTCTGTCATCCATGCTC | chr17 | 48275740 | 48275921 |
| COL1A1 | COL1A1_56 | GGACACACAAGGCCTCTCC | CAGGTGGGCATGGCTCTC | 185 | 69 | GGACACACAAGGCCTCTCCACTTAYTCCTCCGAGRCNN | chr17 | 48276562 | 48276746 |
| COL1A1 | COL1A1_57 | CGAGAGCCATGCCCACC | AATCTCCTGCCCTCGAATTTTGC | 187 | 63 | CGAGAGCCATGCCCACCTGCAGCCCCCCACAGCCCAC | chr17 | 48276728 | 48276914 |
| COL1A1 | COL1A1_58 | CCAGGTTAGAGAAGGGAGGACTG | GACGGGAGCAGCATTAGCAAAC | 162 | 59 | CCAGGTTAGAGAAGGGAGGACTGTGAGGAGTCACGC | chr17 | 48276845 | 48277006 |
| COL1A1 | COL1A1_59 | AGGCCTCCAGCACGGA | GGTGTTGTGCGATGACGTG | 200 | 71 | AGGCCTCCAGCACGGAGGGCCAGCGAGCGCCGAcca | chr17 | 48277012 | 48277211 |
| COL1A1 | COL1A1_6 | GGGCCTTCTTGAGGTTGCC | TCCCCTCCCCTGCAGTTC | 172 | 61 | GGGCCTTCTTGAGGTTGCCAGTCTGCTKGTCCATGTA | chr17 | 48263225 | 48263396 |
| COL1A1 | COL1A1_60 | CGCCCTCGGGGACTTC | CTACTGACAACGCCCCTCTTC | 198 | 61 | CGCCCTCGGGGACTTCGGCGCNNGGGCAGTTCTTGG | chr17 | 48277144 | 48277341 |
| COL1A1 | COL1A1_61 | CGCAAGGCGCGATATAGAGT | GCCACAAAGAGTCTACATGTCTAGG | 187 | 56 | CGCAAGGCGCGATATAGAGTATCCTTGCACTCCCAAA | chr17 | 48278721 | 48278907 |
| COL1A1 | COL1A1_7 | CATCAGGCGCAGGAAGGTC | TCTCGATATAACGGTGCATTGGG | 183 | 62 | CATCAGGCGCAGGAAGGTCNNCTGGATGGCCACATC | chr17 | 48263313 | 48263495 |
| COL1A1 | COL1A1_8 | TCATGTCCCTTCTGAGCACT | ACATGGAGACTGGTGAGACCT | 198 | 55 | TCATGTCCCTTCTGAGCACTGGGCTAGCCCATCTCCTA | chr17 | 48263611 | 48263808 |
| COL1A1 | COL1A1_9 | TCCTTGGGGTTCTTGCTGATGTA | CCTGACTCCATCTTGCCCTG | 176 | 55 | TCCTTGGGGTTCTTGCTGATGTAMCAGTTCTTCTGGG | chr17 | 48263724 | 48263899 |
| COL1A2 | COL1A2_1 | GTACTGGCCACGACTGCAT | CTCCCCCAAACAAGCTGAAGG | 198 | 57 | GTACTGGCCACGACTGCATGCCCGCGCCCGCCAGGTC | chr7 | 94024244 | 94024441 |
| COL1A2 | COL1A2_10 | GGAAAAGGAGTTGGACTTGGC | TGGCGTGGTAAAATGTGACATAAA | 109 | 36 | GGAAAAGGAGTTGGACTTGGCCCTGGACCAATGRYA | chr7 | 94030900 | 94031008 |
| COL1A2 | COL1A2_12 | TGGAATCAAACCACAACAATGGC | AGAGGCATTACAAGCTTTCAGTA | 181 | 46 | TGGAATCAAACCACAACAATGGCACTGCTAAGTTGGT | chr7 | 94033760 | 94033940 |
| COL1A2 | COL1A2_13 | ACTGAAAGCTTGTAATGCCTCTT | AAAAACTTATCACAAAGGTGGAAAAATG | 175 | 38 | ACTGAAAGCTTGTAATGCCTCTTATGTAAAAAGACAG | chr7 | 94033919 | 94034093 |
| COL1A2 | COL1A2_14 | ACCTTAGTGAAATGATGGGTCTCC | GTCAGGCATATTCAGCTTTTGGC | 198 | 40 | ACCTTAGTGAAATGATGGGTCTCCCATTTTCTTAGGGT | chr7 | 94034116 | 94034313 |
| COL1A2 | COL1A2_15 | ACCAAGATTCCCCCATTTTGTCT | AGGCCTATGATGTTTGTGCTATCT | 168 | 44 | ACCAAGATTCCCCCATTTTGTCTGATAGTTTACCAAGA | chr7 | 94034441 | 94034608 |
| COL1A2 | COL1A2_16 | TGATGAGAATAAATACTTTGGAGGGAA | CCAAAAATTAATAGGCATTTTCTCTCTTCT | 193 | 37 | TGATGAGAATAAATACTTTGGAGGGAAGAAGTCACTC | chr7 | 94034895 | 94035087 |
| COL1A2 | COL1A2_17 | TTTTATTTGACCAAACACTATCATGGA | ACTTTTTTGGAGGTCATGGGGAA | 180 | 36 | TTTTATTTGACCAAACACTATCATGGAACAGCATTTTA | chr7 | 94035504 | 94035683 |
| COL1A2 | COL1A2_18 | AGAGTAAAATTGCACTATCAGGAAAAA | AGCAAAAACATTAAAGAAGTTCCATCTCA | 194 | 32 | AGAGTAAAATTGCACTATCAGGAAAAATAATTGTTATA | chr7 | 94037086 | 94037279 |
| COL1A2 | COL1A2_19 | ACAGGTTGGAAACTGAACAAAGC | TGAAACTGAACAAAAATGGAAGCA | 172 | 41 | ACAGGTTGGAAACTGAACAAAGCAAATGATGCCTGTC | chr7 | 94037406 | 94037577 |
| COL1A2 | COL1A2_2 | ACTTGTTTCTCTATTTGTTAATTATTGCTATTGA | AGAGAAGACATCACTGTAGCCAA | 167 | 26 | ACTTGTTTCTCTATTTGTTAATTATTGCTATTGATCnnTC | chr7 | 94026972 | 94027138 |
| COL1A2 | COL1A2_20 | TTCCTGGTGAGAGAGGACGTG | TGTCAAAACTTACAGCAGGACCC | 198 | 45 | TTCCTGGTGAGAGAGGACGTGTTGGTGCCCCTGGYCC | chr7 | 94037508 | 94037705 |
| COL1A2 | COL1A2_21 | ACCTGATCTTCCCTTTATTTTCTTCT | AAAGACCTCACAGAACATTTGGT | 198 | 44 | ACCTGATCTTCCCTTTATTTTCTTCTTAGGGTGCCCGTC | chr7 | 94037619 | 94037816 |
| COL1A2 | COL1A2_22 | TTTCTTACCACCTTCTGCTTTGA | TCTGCAAACACAGTTCCAATCTT | 162 | 43 | TTTCTTACCACCTTCTGCTTTGATTTCRSGRTCCYAWTC | chr7 | 94038053 | 94038214 |

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|---|---|---|---|---|---|---|---|---|---|
| COL1A2 | COL1A2_23 | ATGCTGTTTCATTATTTGCTGGTT | AGACAGTGGCTACTTACAGGAGG | 168 | 48 | ATGCTGTTTCATTATTTGCTGGTTAATTCCTTGGTTTAA | chr7 | 94038582 | 94038749 |
| COL1A2 | COL1A2_24 | GCTGGTTAATTCCTTGGTTTAATTTCCT | CTTCCCCATACTCCACCTTTGTT | 197 | 46 | GCTGGTTAATTCCTTGGTTTAATTTCCTCTTTTAGGRTC | chr7 | 94038599 | 94038795 |
| COL1A2 | COL1A2_25 | ATGGGGTCAAAGAAGAACCGAAA | GCTGTAGAGGCAGCACACATTA | 184 | 42 | ATGGGGTCAAAGAAGAACCGAAATATTCCAATTAACT | chr7 | 94038809 | 94038992 |
| COL1A2 | COL1A2_26 | GCTGCCTCTACAGCCCATC | TTTCAGGATGATGAGAACCACAG | 192 | 53 | GCTGCCTCTACAGCCCATCACCTCCCTAATGGACCACA | chr7 | 94038979 | 94039170 |
| COL1A2 | COL1A2_27 | AAGAGATTTGTCTGCAAGAGAGT | AGCTGGAGAAACTGGAATGAGAA | 189 | 42 | AAGAGATTTGTCTGCAAGAGAGTTTCAACAAATGTTTC | chr7 | 94039484 | 94039672 |
| COL1A2 | COL1A2_28 | ACTCCCTCTTCTTTTGTTCTTTTCA | GGGGTATCATAATCTGCCTCTGG | 197 | 50 | ACTCCCTCTTCTTTTGTTCTTTTCATTAAACAGRGCTCY | chr7 | 94039699 | 94039895 |
| COL1A2 | COL1A2_29 | ACAAACTCTACCTTATCAAAGCCAA | TGCTAAAGCTAATGACACACCCA | 195 | 44 | ACAAACTCTACCTTATCAAAGCCAAGAGATTTCTTTAA | chr7 | 94040134 | 94040328 |
| COL1A2 | COL1A2_3 | ACTACACCAAAATGGAAGCTGTT | AGAAGTAGTGTACTCTTACCTTTCTTAC | 113 | 26 | ACTACACCAAAATGGAAGCTGTTTTTAAATATATATAT | chr7 | 94027615 | 94027727 |
| COL1A2 | COL1A2_30 | TGTCATTAGCTTTAGCATCCTCCT | TAATGCCAGGTGTGATTTGCTC | 197 | 46 | TGTCATTAGCTTTAGCATCCTCCTCCTCTATCTGTTTTT | chr7 | 94040312 | 94040508 |
| COL1A2 | COL1A2_31 | TCTAAGGCTTGAGTATGTAAGTTAAAGTG | AGCCACAAAATAGACTTGATAAGGGT | 187 | 36 | TCTAAGGCTTGAGTATGTAAGTTAAAGTGCCAATATA | chr7 | 94041319 | 94041505 |
| COL1A2 | COL1A2_32 | AGCTTGAGGTTGTGAGAATATGT | GCTGAGGGTAAGAAAGTTGTGGT | 190 | 49 | AGCTTGAGGTTGTGAGAATATGTTGACACTGAGTAAA | chr7 | 94041837 | 94042026 |
| COL1A2 | COL1A2_33 | AGCAGGATTCAACATTGCAAAA | GTGGTTCTTAGATGAATGCTATGTG | 198 | 38 | AGCAGGATTCAACATTGCAAAATCACCGTGGTTAATT | chr7 | 94042305 | 94042502 |
| COL1A2 | COL1A2_34 | ACATCTTAAACTACCTGGCTTGC | ACTTTTGGACTGAAAATGGAGATG | 198 | 42 | ACATCTTAAACTACCTGGCTTGCAGCTAACCATCAGCC | chr7 | 94042944 | 94043141 |
| COL1A2 | COL1A2_35 | GGCCATCTCCATTTTCAGTCCAA | ACAGCTCAATAGGCTGACCAAA | 198 | 44 | GGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAC | chr7 | 94043115 | 94043312 |
| COL1A2 | COL1A2_36 | CCCAAACTCAATTATTAGCAAATCTCC | AGCAGTGGGGTATTAAACAGGG | 200 | 41 | CCCAAACTCAATTATTAGCAAATCTCCTGAACRTAGCC | chr7 | 94043461 | 94043660 |
| COL1A2 | COL1A2_37 | TGCCAGGTTTATTTCACTCTTTCC | AAAAACACATTGCCAGAGTTTATGA | 196 | 35 | TGCCAGGTTTATTTCACTCTTTCCAAATTTTTCAAATAT | chr7 | 94044434 | 94044629 |
| COL1A2 | COL1A2_38 | CACTGAAAGTGATGAATGGTGCAA | CTGGGCCAAACCAGCAATATAGA | 187 | 48 | CACTGAAAGTGATGAATGGTGCAACACTTCTTCTAATC | chr7 | 94045668 | 94045854 |
| COL1A2 | COL1A2_39 | TTGATTCTTCATTTTCTTCTTTCTCCAC | TTTTCTCCCTTGCCTCCAGGTAT | 166 | 46 | TTGATTCTTCATTTTCTTCTTTCTCCACTAAAATTGATTT | chr7 | 94046977 | 94047142 |
| COL1A2 | COL1A2_40 | ACATGTGTTTGACTCAAGGGTG | ATCCTTGTGCAGCCTTCTTTACT | 188 | 48 | ACATGTGTTTGACTCAAGGGTGAACCTGRTGTKGTTSC | chr7 | 94047018 | 94047205 |
| COL1A2 | COL1A2_41 | ACTGAAGGTATCATAGCATCTTCTGTA | CACACGAGCACCATCTCTG | 165 | 35 | ACTGAAGGTATCATAGCATCTTCTGTAAAAAAGAAAA | chr7 | 94047703 | 94047867 |
| COL1A2 | COL1A2_43 | CAGAGATGGTGCTCGTGTG | ATAGACCCAGGAGAGAAAGGAAT | 157 | 29 | CAGAGATGGTGCTCGTGTGRRTAGAATTTTGTTTGTAT | chr7 | 94047849 | 94048005 |
| COL1A2 | COL1A2_44 | ATCCAACCAGAGTGCAGTGAAAG | CTCCAGCAGGACCAGGG | 162 | 43 | ATCCAACCAGAGTGCAGTGAAAGTGTTCAGTCACTGT | chr7 | 94048688 | 94048849 |
| COL1A2 | COL1A2_45 | TGACAAGGTTCACTTTTGATGATACG | TAGGGAAGGCGGGAAATTTTAGA | 176 | 45 | TGACAAGGTTCACTTTTGATGATACGGGGTGTTNNTA | chr7 | 94048745 | 94048920 |
| COL1A2 | COL1A2_46 | TGCCCCTGGTCCTGCT | AGCATTTGTTTCCTGCTGCTCTA | 189 | 44 | TGCCCCTGGTCCTGCTGGAGCCACAGGTGACCRGGTA | chr7 | 94048830 | 94049018 |
| COL1A2 | COL1A2_47 | TCTGTCCACCACTGTTCTCTCT | TGTCTAAACATTGTGAGGTGTGA | 194 | 47 | TCTGTCCACCACTGTTCTCTCTCCCTYCCAGTTCTTTGA | chr7 | 94049458 | 94049651 |
| COL1A2 | COL1A2_48 | TGGGTCATTTTGTATACTCACACCT | ACTCCCCAACTTAGGATGTTTTCA | 196 | 41 | TGGGTCATTTTGTATACTCACACCTCACAATGTTTAGA | chr7 | 94049612 | 94049807 |
| COL1A2 | COL1A2_49 | GTCGGAATACCAGAGCTGTAACT | ATCTAATGGGTAGCTGCTGTGTG | 192 | 47 | GTCGGAATACCAGAGCTGTAACTGTTTATTTCCAACAC | chr7 | 94049815 | 94050006 |
| COL1A2 | COL1A2_5 | TCACTGGAAATTACTTCTTAGGCAT | TGCCAGTTCCTGTAGTTTCTAACAT | 169 | 40 | TCACTGGAAATTACTTCTTAGGCATTTATTATTGTCCTC | chr7 | 94028304 | 94028472 |
| COL1A2 | COL1A2_50 | GCGGGAATGATCCACTTGAAGAA | TGAAAAAAGAAAAGCGGCGAGAG | 178 | 44 | GCGGGAATGATCCACTTGAAGAAAAGAGTAGCATTTA | chr7 | 94050238 | 94050415 |
| COL1A2 | COL1A2_51 | ACCCAAATTCTTGGAGTTGATGT | CCAGGCCTTTTGGCTAGAGTAAAT | 162 | 46 | ACCCAAATTCTTGGAGTTGATGTTGACTGTGGAATTCT | chr7 | 94051155 | 94051316 |
| COL1A2 | COL1A2_52 | CCCCAAATGGCCAGGGTATTATT | CCCTTCTTTCCCAGCAGGAC | 177 | 46 | CCCCAAATGGCCAGGGTATTATTTTATTGCATCACATT | chr7 | 94052140 | 94052316 |
| COL1A2 | COL1A2_53 | CAGGCCCTTGGTGATTAACAGAA | AGGGGGACCAACTGCAC | 169 | 52 | CAGGCCCTTGGTGATTAACAGAAAGGAAATGACCTTC | chr7 | 94052217 | 94052385 |
| COL1A2 | COL1A2_54 | CTGGTCCTGCTGGGAAAGAAG | TCAGCATAAGGTATTAAGAAAGAGGAGT | 179 | 48 | CTGGTCCTGCTGGGAAAGAAGGGCTTCGTRGTCCTCR | chr7 | 94052294 | 94052472 |
| COL1A2 | COL1A2_55 | AAGCCAACCTGTGTTATCACCTA | ATACTGTCAAGCACTCACCACAG | 189 | 49 | AAGCCAACCTGTGTTATCACCTAGGGTCTTACCCATAA | chr7 | 94053585 | 94053773 |
| COL1A2 | COL1A2_56 | AGGTCCTCAGGGTCTTCTTGG | TCACATTTGAAGTGGCAGCTTTT | 162 | 47 | AGGTCCTCAGGGTCTTCTTGGTGCTCCTGGTATTCTGC | chr7 | 94053665 | 94053826 |
| COL1A2 | COL1A2_57 | TTCCATCGAATAAGGGGAATGTC | TACAAACCAAGTGTTGGACTCAC | 178 | 52 | TTCCATCGAATAAGGGGAATGTCATTTTATCTTCTCTG | chr7 | 94054382 | 94054559 |
| COL1A2 | COL1A2_58 | TAGCTACAACATAGGGGCTGGTA | AGCATCAATCTGGGTTGCATTTT | 188 | 48 | TAGCTACAACATAGGGGCTGGTAGGCAGCAGAGCCTC | chr7 | 94054851 | 94055038 |
| COL1A2 | COL1A2_59 | AAAATGCAACCCAGATTGATGCT | CTGCACTGAGGGACTGGTATTC | 186 | 49 | AAAATGCAACCCAGATTGATGCTAAGCTTCATTTTGCC | chr7 | 94055016 | 94055201 |
| COL1A2 | COL1A2_6 | ACCACATATAATTCTTAGGTTTCTACAGG | AGCTAAAAGTTAGCAATACGTAAGACAC | 194 | 53 | ACCACATATAATTCTTAGGTTTCTACAGGGCCTGTCTA | chr7 | 94029440 | 94029633 |

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|---|---|---|---|---|---|---|---|---|---|
| COL1A2 | COL1A2_60 | CTTCACTTCTGACTTCCCCACAC | TGTTAGTGTTGCAAAGAAATCTTCAG | 187 | 47 | CTTCACTTCTGACTTCCCCACACTTGGGGATGGTGGA( | chr7 | 94055214 | 94055400 |
| COL1A2 | COL1A2_61 | CGGTAAGTCTTATCCATCCTTCTGT | TATGTGCGAGATGGCTACAGTTT | 172 | 47 | CGGTAAGTCTTATCCATCCTTCTGTTTCTTTATAGGGC( | chr7 | 94055700 | 94055871 |
| COL1A2 | COL1A2_62 | ATGTCTCTTGACATGTGCTCTG | CACTGCTCGCTTTAGCCTCTATT | 165 | 45 | ATGTCTCTTGACATGTGCTCTGAAAGTGTGATTTTCCT | chr7 | 94056267 | 94056431 |
| COL1A2 | COL1A2_63 | CATGTACCTGGTGTCTGTCTTCC | ACATTCCTTAGGTCCGTGATCTT | 186 | 49 | CATGTACCTGGTGTCTGTCTTCCTTAGGGCCCTGCTKG | chr7 | 94056473 | 94056658 |
| COL1A2 | COL1A2_64 | AAATCTGCTGCCATGGATGTCTC | TTGGGTCTGAGAGAAGGTGCT | 198 | 46 | AAATCTGCTGCCATGGATGTCTCTCACTGTAAMAAAA | chr7 | 94056866 | 94057063 |
| COL1A2 | COL1A2_65 | GTAAGCGGTGGTGGTTATGACTT | GCTGGGTTCTTTCTAGAGCCTTC | 173 | 49 | GTAAGCGGTGGTGGTTATGACTTTGGTTAYGATGGAC | chr7 | 94056978 | 94057150 |
| COL1A2 | COL1A2_66 | CCCAAGGACTATGAAGTTGATGC | AAAGCTCAACTTGTGAGAAGGGT | 189 | 50 | CCCAAGGACTATGAAGTTGATGCTACTCTGAAGTCTC | chr7 | 94057059 | 94057247 |
| COL1A2 | COL1A2_67 | AGTTATTATTAGAATCTGTGTTCTGCTCA | AGTTCTTGGCTGGGATGTTTTCA | 188 | 37 | AGTTATTATTAGAATCTGTGTTCTGCTCAATGAGAAGT | chr7 | 94057537 | 94057724 |
| COL1A2 | COL1A2_69 | GGCCCAACCTGAAAACATCC | GTGTTTGTGGGATTCCTCACCTG | 117 | 51 | GGCCCAACCTGAAAACATCCCAGCCAAGAACTGGTAT | chr7 | 94057693 | 94057809 |
| COL1A2 | COL1A2_7 | TCAAAAACATTGCCCTCTTTTAAATAAC | GCCAAGTCCAACTCCTTTTCC | 171 | 26 | TCAAAAACATTGCCCTCTTTTAAATAACAACAGAAAAA | chr7 | 94030750 | 94030920 |
| COL1A2 | COL1A2_71 | AACCTGAAAACATCCCAGCCAA | GAGATTAAAATGCAGATAATTAACAAACAGTCC | 174 | 43 | AACCTGAAAACATCCCAGCCAAGAACTGGTATAGGAC | chr7 | 94057698 | 94057871 |
| COL1A2 | COL1A2_72 | ACTCTTAGTATCTGAGTCCTTCTCCA | TTCTTGCAGTGGTAGGTGATGTT | 167 | 42 | ACTCTTAGTATCTGAGTCCTTCTCCACTTAACTGGAAT | chr7 | 94058443 | 94058609 |
| COL1A2 | COL1A2_73 | AGGAGTGACTTCCAAGGAAATGG | CCTCAGCAACAAGTTCAACATCA | 182 | 48 | AGGAGTGACTTCCAAGGAAATGGCTACCCAACTTGCC | chr7 | 94058517 | 94058698 |
| COL1A2 | COL1A2_74 | CATCACCTACCACTGCAAGAACA | CCACTTCCCAAAGCTATTCCCAT | 194 | 44 | CATCACCTACCACTGCAAGAACAGCATTGCATACATG( | chr7 | 94058589 | 94058782 |
| COL1A2 | COL1A2_75 | CATGCCAAACAGTGGTTCTTATT | GCACCACCGATGTCCAAAG | 198 | 35 | CATGCCAAACAGTGGTTCTTATTAAATCAAAGGTTCA( | chr7 | 94059462 | 94059659 |
| COL1A2 | COL1A2_76 | TGATGCTTTGTGTATCTATTTTCTTCTC | CTGGGCCAATGTCCACAAAGA | 170 | 38 | TGATGCTTTGTGTATCTATTTTCTTCTCTTTAAACAGAA | chr7 | 94059522 | 94059691 |
| COL1A2 | COL1A2_77 | ACCTTTGGACATCGGTGGTG | GCAGAAGAAATGGAAGGATTCAGC | 174 | 34 | ACCTTTGGACATCGGTGGTGCTGACCAKGAATTCTTT( | chr7 | 94059639 | 94059812 |
| COL1A2 | COL1A2_8 | TCAAAAACATTGCCCTCTTTTAAATAAC | GGGCCAAGTCCAACTCCTTT | 173 | 27 | TCAAAAACATTGCCCTCTTTTAAATAACAACAGAAAAA | chr7 | 94030750 | 94030922 |
| COL3A1 | COL3A1_1 | TTGATGGTGCTACTTTGAACTGC | TCCCATAAAGTTTCTTGAAATCAGTACC | 186 | 41 | TTGATGGTGCTACTTTGAACTGCTTTTCTTTTCTCCTTT | chr2 | 189839144 | 189839329 |
| COL3A1 | COL3A1_10 | GCTTTGAAGCATGGATAAAGTGT | AAAAATGAGGAAGAAAACACCACCA | 162 | 43 | GCTTTGAAGCATGGATAAAGTGTATTTTGCATTCATTT | chr2 | 189852738 | 189852899 |
| COL3A1 | COL3A1_11 | GAGTAAAATTTGCTGATTACATTCACAATCC | ACTTACTGAAGGACCAGCTTGC | 171 | 36 | GAGTAAAATTTGCTGATTACATTCACAATCCTGATTTC | chr2 | 189853205 | 189853375 |
| COL3A1 | COL3A1_14 | GCAAGCTGGTCCTTCAGTAAGT | ACAATTGAAAGAGTCCAAAAGACTCAA | 182 | 28 | GCAAGCTGGTCCTTCAGTAAGTRRCAATTAAATTTATA | chr2 | 189853354 | 189853535 |
| COL3A1 | COL3A1_15 | TCTATTCATTTTTTATTTCCTTATTTTCAGGG | TTCTGGGATTCTGACATAAAGCAT | 171 | 35 | TCTATTCATTTTTTATTTCCTTATTTTCAGGGCCCTCCA( | chr2 | 189854092 | 189854262 |
| COL3A1 | COL3A1_16 | CCATTTTGCTTATTGGCTACAATGTATTT | ACATAATAGTTTTCAAGCTAAGATTATTCCA | 185 | 39 | CCATTTTGCTTATTGGCTACAATGTATTTTYTCATACAT | chr2 | 189854750 | 189854934 |
| COL3A1 | COL3A1_17 | CAATGGAATTAAACTTAAAAACAGAAAGTGT | AGCCCAGTGGAATACCTTGTAAA | 192 | 33 | CAATGGAATTAAACTTAAAAACAGAAAGTGTTTTACTA | chr2 | 189854939 | 189855130 |
| COL3A1 | COL3A1_18 | TTTAATAATTTTGCTGGTTTTATACATTTCCT | GTTGTGATTTACCTTTAATCCAGGAGC | 100 | 38 | TTTAATAATTTTGCTGGTTTTATACATTTCCTAGGGCTT | chr2 | 189855696 | 189855795 |
| COL3A1 | COL3A1_19 | GGTTTTATACATTTCCTAGGGCTTCG | CAGAAAACAAGTTAAGGCTCACAA | 168 | 32 | GGTTTTATACATTTCCTAGGGCTTCGATGGACGAAAT( | chr2 | 189855711 | 189855878 |
| COL3A1 | COL3A1_2 | TCAGCAAAACCTAAGGAAACTTCAC | GGGGCAGTCTAATTCTTGATCGT | 192 | 43 | TCAGCAAAACCTAAGGAAACTTCACRTCATYTAACTTG | chr2 | 189849440 | 189849631 |
| COL3A1 | COL3A1_20 | ATTTTATATGTATCTAGGGTGAAAATGGTC | TTGACATGTGTAAGAACAGTTGGG | 162 | 36 | ATTTTATATGTATCTAGGGTGAAAATGGTCTTCCAGG( | chr2 | 189856196 | 189856357 |
| COL3A1 | COL3A1_22 | CCACCCCAACTGTTCTTACACAT | ACAGCCTGAAACTTTACTGAGGC | 197 | 46 | CCACCCCAACTGTTCTTACACATGTCAAGATTAGAGTA | chr2 | 189856330 | 189856526 |
| COL3A1 | COL3A1_23 | ATTACTCATGACCAGCCATTCAG | TCCACAATCCATAACTTCTCATTACCC | 163 | 40 | ATTACTCATGACCAGCCATTCAGAATTAAAAGGATATT | chr2 | 189856850 | 189857012 |
| COL3A1 | COL3A1_24 | TGCATAAATATCTTCTTTACTTTATATGTGCT | ACATGTTTACCTTAGCACCAGGG | 168 | 39 | TGCATAAATATCTTCTTTACTTTATATGTGCTCACTTAT | chr2 | 189857509 | 189857676 |
| COL3A1 | COL3A1_25 | CTCCTGGTCCTCCTGGAACT | GATAAAAGCTATCCATTTGACTGATTAAAAAA | 162 | 40 | CTCCTGGTCCTCCTGGAACTGCCGGATTCCCTGGATCC( | chr2 | 189857617 | 189857778 |
| COL3A1 | COL3A1_26 | TGAAGGGTGAAGTGGCTAAGTGA | TACTTACAGGAGGACCTTGAGCA | 174 | 51 | TGAAGGGTGAAGTGGCTAAGTGAGTAGAAGTGGTAA | chr2 | 189858019 | 189858192 |
| COL3A1 | COL3A1_27 | CCATTAGGGTGAAGTTGGACCTG | AGCACATGCTTTCATGGAGTAAG | 196 | 48 | CCATTAGGGTGAAGTTGGACCTGCAGGGTCTCCTGGT | chr2 | 189858080 | 189858275 |
| COL3A1 | COL3A1_28 | TCGATACATTTATTTTCACACAAACAAC | AGCCAGTAATGTGTGGATGAGAT | 184 | 38 | TCGATACATTTATTTTCACACAAACAACTTCAAATATA | chr2 | 189858674 | 189858857 |
| COL3A1 | COL3A1_29 | GGCTTCTTTTGCATTTTGCATGAC | GCAGTCCAGGAGCACCATTAG | 194 | 46 | GGCTTCTTTTGCATTTTGCATGACAATAGATTTGTGAT | chr2 | 189858854 | 189859047 |
| COL3A1 | COL3A1_3 | CTGTTGAAGGAGGATGTTCCCAT | GTGGGCAAACTGCACAACATTC | 189 | 46 | CTGTTGAAGGAGGATGTTCCCATCTTGGTCAGTCCTA | chr2 | 189849486 | 189849674 |
| COL3A1 | COL3A1_30 | CCTGGACTGATGGGAGCC | AAATTCAACTGAACAGGAGCAAAA | 173 | 45 | CCTGGACTGATGGGAGCCCGGGGTCCTCCAGGACCA( | chr2 | 189858984 | 189859156 |

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|---|---|---|---|---|---|---|---|---|---|
| COL3A1 | COL3A1_31 | TGATTTGTTAGTCGAATCCTCCCT | AGTTCAAAGTTTTTACCTGTTTACTTTCT | 191 | 40 | TGATTTGTTAGTCGAATCCTCCCTGTGTTTCAACCAAG | chr2 | 189859212 | 189859402 |
| COL3A1 | COL3A1_32 | GAAAGTAAACAGGTAAAAACTTTGAACTAAA | CCCCATGGAAAACGTACCCT | 200 | 42 | GAAAGTAAACAGGTAAAAACTTTGAACTAAATTCAGT | chr2 | 189859375 | 189859574 |
| COL3A1 | COL3A1_33 | ATTCCAGGTGTTCCAGGAGCTAA | AAATTGGCTGTCTCACCCTGAAG | 180 | 48 | ATTCCAGGTGTTCCAGGAGCTAAAGGCGAAGATGGC/ | chr2 | 189859462 | 189859641 |
| COL3A1 | COL3A1_34 | TGCCACTCAAGAATTATGAAAAAGAA | CAAGAACTGCCCATTTGTGGTG | 182 | 42 | TGCCACTCAAGAATTATGAAAAAGAATTGAAATCCTT | chr2 | 189859702 | 189859883 |
| COL3A1 | COL3A1_35 | TGTTGCTATCTAGGTTAGTGAAGGC | ACAAATGTTTCTCTGTACCCTCAT | 178 | 48 | TGTTGCTATCTAGGTTAGTGAAGGCtattttaatttttttaa | chr2 | 189860357 | 189860534 |
| COL3A1 | COL3A1_36 | TGCAGGGCCCAGAGGA | TCTGATTGATTTAAGTTGCTTTTGATCT | 162 | 44 | TGCAGGGCCCAGAGGAGCTGCTGGAGAACCTGGCAC | chr2 | 189860450 | 189860611 |
| COL3A1 | COL3A1_37 | TTCATTTTAAATCACCTAACAACTGACT | ACACACACACACACTCAAGGATA | 179 | 42 | TTCATTTTAAATCACCTAACAACTGACTTCTTTACTTCA | chr2 | 189860811 | 189860989 |
| COL3A1 | COL3A1_38 | GCATGCTTTAATCTTCTCTTTATCAAACC | TGAAGAAATTAATGAAGGAACTCACATC | 180 | 44 | GCATGCTTTAATCTTCTCTTTATCAAACCTTTATTAATG | chr2 | 189861068 | 189861247 |
| COL3A1 | COL3A1_39 | GGGAAGTCAAGGAGAAAGTGGT | TGAAGAGGAGACTGAGTTTTGAC | 198 | 46 | GGGAAGTCAAGGAGAAAGTGGTCGACCAGGTCCTCC | chr2 | 189861123 | 189861320 |
| COL3A1 | COL3A1_4 | CAAGAATTAGACTGCCCCAACCC | ACATGGCTATTTGATGAACATGACT | 189 | 39 | CAAGAATTAGACTGCCCCAACCCAGAAATTCCATTTG | chr2 | 189849614 | 189849802 |
| COL3A1 | COL3A1_40 | AGTTATTGCCCTTTGAGGATTAGT | AGTCAGAAGGTTGGAGATGAACG | 168 | 46 | AGTTATTGCCCTTTGAGGATTAGTAAATACCGACCAC | chr2 | 189861843 | 189862010 |
| COL3A1 | COL3A1_41 | CCAACCTTCTGACTTCTCTCTGT | CCCACCTCCACCCTATTTTCATC | 167 | 44 | CCAACCTTCTGACTTCTCTCTGTAATCTGTATTATTTCT | chr2 | 189861997 | 189862163 |
| COL3A1 | COL3A1_42 | TCACATCACTACTTTTATAATTAAGCAACA | AGTCAGATATGCCGTGACATTTA | 198 | 38 | TCACATCACTACTTTTATAATTAAGCAACAGRCCTGTT | chr2 | 189862321 | 189862518 |
| COL3A1 | COL3A1_43 | GCTTTTCTATAAGCCATGTTTGAGGT | CAAACAGTGTGTATTCTTTTTGTTTCTG | 166 | 38 | GCTTTTCTATAAGCCATGTTTGAGGTAATTACCTAATA | chr2 | 189862935 | 189863100 |
| COL3A1 | COL3A1_44 | atatttACATAAAATGCACTCTGATATGGG | ACTACTAATCAATTGCTCTATAACCTGCT | 162 | 41 | atatttACATAAAATGCACTCTGATATGGGCCTAATCAT | chr2 | 189863343 | 189863504 |
| COL3A1 | COL3A1_45 | GGCCTGATTCAAAATGATGCAAGT | GTGGAGTTACCTTTCCTCCTTCG | 195 | 49 | GGCCTGATTCAAAATGATGCAAGTTAAGGTGCTTTGT | chr2 | 189863925 | 189864119 |
| COL3A1 | COL3A1_46 | TCACAGGGTGATGCTGGT | AGCACCCTGAAAATAAGTGAGAA | 197 | 49 | TCACAGGGTGATGCTGGTRCCCCTGGTGAACGTGGA | chr2 | 189864005 | 189864201 |
| COL3A1 | COL3A1_47 | CGAAGGAGGAAAGGTAACTCCAC | TTCCAAGACCTCCTCTTTCTCCA | 184 | 46 | CGAAGGAGGAAAGGTAACTCCACAGCATTCCATTCAC | chr2 | 189864097 | 189864280 |
| COL3A1 | COL3A1_48 | CACTTATTTTCAGGGTGCTGCTG | ACTTTCCAGGAGTGTTGCTTTTT | 198 | 46 | CACTTATTTTCAGGGTGCTGCTGGTCCTCCTGGGCCAC | chr2 | 189864183 | 189864380 |
| COL3A1 | COL3A1_49 | TGAGAGTTACTCCTCTTCTTGGC | TAGATAAGGCCTGCTTCTCCTCA | 167 | 47 | TGAGAGTTACTCCTCTTCTTGGCTGATTTTCACTGAAG | chr2 | 189864492 | 189864658 |
| COL3A1 | COL3A1_5 | TGCAAATTCTGTGTCTTGTTTAACTTGT | AGCTCAAATCTAGAAAAAGCAAACTCT | 177 | 36 | TGCAAATTCTGTGTCTTGTTTAACTTGTTTCTTTTCCAT | chr2 | 189849877 | 189850053 |
| COL3A1 | COL3A1_50 | AGGTATCTATGTCTATATACTTTCTGTTTGAT | AGGTAGTATTAAGGGTTACCTTATCTCCAG | 163 | 37 | AGGTATCTATGTCTATATACTTTCTGTTTGATTAATGC/ | chr2 | 189866033 | 189866195 |
| COL3A1 | COL3A1_51 | ttatttCCTCTAGGGTCCTACTGGTC | CACCTTCACCCTGGAAAAAGAGA | 162 | 46 | ttatttCCTCTAGGGTCCTACTGGTCCTATTGGTCCTCCT | chr2 | 189866110 | 189866271 |
| COL3A1 | COL3A1_52 | AGGTAACCCTTAATACTACCTGGA | TAGCTACTGTCTGTATGGGGTT | 196 | 43 | AGGTAACCCTTAATACTACCTGGAWATAAAAAGAAA/ | chr2 | 189866175 | 189866370 |
| COL3A1 | COL3A1_53 | TTTCCTGCCTAAAGGAGATGACG | ATAGAGATCCTGGGCTATGGGAC | 166 | 47 | TTTCCTGCCTAAAGGAGATGACGCACACTTCACTGTG/ | chr2 | 189866961 | 189867126 |
| COL3A1 | COL3A1_54 | AGCTGAGAGATTGCTGTTGTTGT | agacagaGAAAGAGGAAGGAACT | 166 | 53 | AGCTGAGAGATTGCTGTTGTTGTTGCATGTAGGGACA | chr2 | 189867649 | 189867814 |
| COL3A1 | COL3A1_55 | GGCTTAATGCTTTTCCCAAATTTTGATT | TCTCAAATGCAGCTTTTATACAGGT | 196 | 38 | GGCTTAATGCTTTTCCCAAATTTTGATTTTGGTRCTATT | chr2 | 189868069 | 189868264 |
| COL3A1 | COL3A1_56 | AGGGGAAACACAAACCATAAATGAC | ACTTTAACAATTACTTACATTACTACCAGGA | 198 | 37 | AGGGGAAACACAAACCATAAATGACTTTCAGGTACAA | chr2 | 189868334 | 189868531 |
| COL3A1 | COL3A1_57 | TATTACCATTTCACAGGGTGCTG | ACTAGAGAAATAAGTAGCAATGTGTAAGTTT | 170 | 40 | TATTACCATTTCACAGGGTGCTGCTGGCTTCCCTGGTG | chr2 | 189868444 | 189868613 |
| COL3A1 | COL3A1_58 | ACTTACACATTGCTACTTATTTCTCTAGT | CCAGTGTTACCCGCAGGAC | 197 | 38 | ACTTACACATTGCTACTTATTTCTCTAGTAASTCTCAAA | chr2 | 189868585 | 189868781 |
| COL3A1 | COL3A1_59 | ATTTGTAGGGTAACCCAGGACCC | CATCACCTTTTGGTCCAGACACT | 123 | 62 | ATTTGTAGGGTAACCCAGGACCCCCAGGTCCCAGCGC | chr2 | 189868700 | 189868822 |
| COL3A1 | COL3A1_6 | TGTGAATCACCAGGATTTTTCACTATT | CTGAGGACCAGTAGGGCATGATT | 166 | 47 | TGTGAATCACCAGGATTTTTCACTATTTAATTTATTTTT | chr2 | 189850339 | 189850504 |
| COL3A1 | COL3A1_60 | GGTCCTGCGGGTAACACT | ATGTGACAGTGTTTTTCTCTAATCG | 188 | 47 | GGTCCTGCGGGTAACACTGGTGCTCCTGGCAGCCCTG | chr2 | 189868762 | 189868949 |
| COL3A1 | COL3A1_61 | CACTGTCACATAAAGATGAGCTAAGT | GGCTACCAAAGGAAGGAAGAGTG | 198 | 53 | CACTGTCACATAAAGATGAGCTAAGTCTTCATTATCTG | chr2 | 189868939 | 189869136 |
| COL3A1 | COL3A1_63 | TTTCCCATAGCAGGCATAGTTTT | TTAGCTCCTGGTTTCCCACTTTC | 174 | 27 | TTTCCCATAGCAGGCATAGTTTTAATTTTAAAATTCAA | chr2 | 189869928 | 189870101 |
| COL3A1 | COL3A1_64 | GTATACAGGGTGAAAGTGGGAAAC | TGCTACTCACATCTCTTCCAGGT | 126 | 56 | GTATACAGGGTGAAAGTGGGAAACCAGGAGCTAAYG | chr2 | 189870068 | 189870193 |
| COL3A1 | COL3A1_66 | GAGAACGTGGTCCCCCTG | TGTGGCCATATTTACACTCTTAGACA | 173 | 45 | GAGAACGTGGTCCCCCTGGACCCCAGGGTCTTCCTGC | chr2 | 189870113 | 189870285 |
| COL3A1 | COL3A1_67 | GGAAGGTTTCAAGAAATTTTATTTCCTTTCTC | CCACGATCACCCTGTGAACAAAT | 195 | 37 | GGAAGGTTTCAAGAAATTTTATTTCCTTTCTCATTTTTT | chr2 | 189870887 | 189871081 |
| COL3A1 | COL3A1_68 | AAGTGATCATCATGTTTATTTTGTACCT | CTGCTTTTGGGAACTCACACTTT | 170 | 51 | AAGTGATCATCATGTTTATTTTGTACCTATGAATTTGTT | chr2 | 189871027 | 189871196 |

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|---|---|---|---|---|---|---|---|---|---|
| COL3A1 | COL3A1_69 | TGATCGTGGTGAAAATGGCTCT | AGATCTGACATTCTACCTTCTACCT | 191 | 50 | TGATCGTGGTGAAAATGGCTCTCCTGGTGCCCCTGGC | chr2 | 189871073 | 189871263 |
| COL3A1 | COL3A1_7 | GTATTCCAGGACAACCAGGGTC | ACACTGAATCAGAGAACAGATACAA | 197 | 41 | GTATTCCAGGACAACCAGGGTCCCCTGGTTCTCCTGG | chr2 | 189850428 | 189850624 |
| COL3A1 | COL3A1_70 | ACTAgTTCcGTGTATGTCTTCTCA | TTTTCCTGAACACGcTGGAAAAT | 196 | 41 | ACTAgTTCcGTGTATGTCTTCTCAATTGAATGTTTTCAT | chr2 | 189871619 | 189871814 |
| COL3A1 | COL3A1_71 | ttttatttttCCAATATGTATGTGTGTATATGACT | AACCTGGGGCACCTGGATTA | 162 | 44 | ttttatttttCCAATATGTATGTGTGTATATGACTTCAATTC | chr2 | 189872167 | 189872328 |
| COL3A1 | COL3A1_72 | AAACAGGTGAACGTGGAGC | GCCTTCAAATCCATTTCTCATCTC | 198 | 38 | AAACAGGTGAACGTGGAGCTGCTGGCATCAAAGGAC | chr2 | 189872257 | 189872454 |
| COL3A1 | COL3A1_73 | TGTACAGTTTCCCAGTGCTTTTT | TGCAGACATCTGAAACATGTGGA | 165 | 50 | TGTACAGTTTCCCAGTGCTTTTTAAGGCCTTCACTCCT | chr2 | 189872550 | 189872714 |
| COL3A1 | COL3A1_74 | CCACATGTTTCAGATGTCTGCATT | CCTCTTTCACCTCTGTTACCTCG | 169 | 50 | CCACATGTTTCAGATGTCTGCATTTCAGAAAGATATTC | chr2 | 189872693 | 189872861 |
| COL3A1 | COL3A1_75 | TGATGTCATGATACTTTCTTAGGGAC | GCGCTGTGTTTCTGAAAATTGGA | 198 | 46 | TGATGTCATGATACTTTCTTAGGGACCTGTTGGACCCA | chr2 | 189872739 | 189872936 |
| COL3A1 | COL3A1_76 | TTCTTAGAGTGGCGACTGAATGT | AAAACCGCCAGCTTTTTCACC | 181 | 56 | TTCTTAGAGTGGCGACTGAATGTGCATACCTCAATGA | chr2 | 189873592 | 189873772 |
| COL3A1 | COL3A1_77 | GGCAACCAGGCCCTCC | TGAGTGAAGTCATAATCTCATCGGT | 171 | 52 | GGCAACCAGGCCCTCCTGGACCTCCTGGTGCCCCTGG | chr2 | 189873669 | 189873839 |
| COL3A1 | COL3A1_78 | GCTGGGATTGGAGGTGAAAAAG | TTCAGGATGGCAGAATTTCAGGT | 198 | 42 | GCTGGGATTGGAGGTGAAAAAGCTGGCGGTTTTKCC | chr2 | 189873740 | 189873937 |
| COL3A1 | COL3A1_79 | GCCTCATTAGTCCTGATGGTTCT | TGAAAGTAGATGTTTTTTCGTTCCCA | 174 | 41 | GCCTCATTAGTCCTGATGGTTCTCGTAAAAACCCCGCY | chr2 | 189873864 | 189874037 |
| COL3A1 | COL3A1_8 | ACATCTTTTGGCACACAAAAACCT | GGATAGCCTGCGAGTCCT | 195 | 38 | ACATCTTTTGGCACACAAAAACCTATCAGTAGACAGTA | chr2 | 189851661 | 189851855 |
| COL3A1 | COL3A1_80 | AGGTAAACAAACAAAATCACTTTATTACTGG | CCAGTGTTTCCGTGGAACATTCA | 193 | 36 | AGGTAAACAAACAAAATCACTTTATTACTGGATTTTAT | chr2 | 189874833 | 189875025 |
| COL3A1 | COL3A1_81 | TTGACCCTAACCAAGGATGCAAA | CCTTTCCTACCTGAAAACCACCA | 186 | 43 | TTGACCCTAACCAAGGATGCAAATTGGATGCTATCAA | chr2 | 189874916 | 189875101 |
| COL3A1 | COL3A1_82 | CTGGTGGACAGATTCTAGTGCTG | accaacctaGTAACTTTGCTTTGTG | 164 | 38 | CTGGTGGACAGATTCTAGTGCTGAGAAGAAACACGTT | chr2 | 189875022 | 189875185 |
| COL3A1 | COL3A1_83 | TGCATACACATACTACATGAATCCCTC | GCAGTGATATGTGATGTTCTGGGA | 185 | 43 | TGCATACACATACTACATGAATCCCTCRCGTGCAGTTA | chr2 | 189875294 | 189875478 |
| COL3A1 | COL3A1_84 | TTTAGCTACGGCAATCCTGAACT | TCACCTTCATTTGACCCCATCAG | 185 | 46 | TTTAGCTACGGCAATCCTGAACTTCCTGAAGATGTCCT | chr2 | 189875374 | 189875558 |
| COL3A1 | COL3A1_85 | TAGCATTGCATACATGGATCAGG | AAAATGCTGACTGCTTTATGACC | 180 | 42 | TAGCATTGCATACATGGATCAGGCCAGTGGAAATGTA | chr2 | 189875484 | 189875663 |
| COL3A1 | COL3A1_86 | GTCAGAGTTGTCTAAGTAATTGTAATGTC | GCCAACGTCCACACCAAATTC | 189 | 41 | GTCAGAGTTGTCTAAGTAATTGTAATGTCATGATCATC | chr2 | 189876294 | 189876482 |
| COL3A1 | COL3A1_87 | AGCAAAACAGTCTTTGAATATCGAAC | ACAAGATTAGAACAAGAGGAACACA | 199 | 38 | AGCAAAACAGTCTTTGAATATCGAACACGCARGGCTG | chr2 | 189876372 | 189876570 |
| COL3A1 | COL3A1_9 | CCTTGCCACAGAACTATTCTCCC | ACTGAATTCCTAGAAGAGCAACCA | 180 | 42 | CCTTGCCACAGAACTATTCTCCCCAGTATGATTCATAT | chr2 | 189851774 | 189851953 |
| COL5A1 | COL5A1_10 | CTTCCTGGTCTCCATCTACAACG | GGGACAGTTGCCCAGAAGTG | 179 | 61 | CTTCCTGGTCTCCATCTACAACGAGCAGGGTATCCAG | chr9 | 137591819 | 137591997 |
| COL5A1 | COL5A1_11 | GCTTGAGCTGGCATCTGTGA | CATTGATGTCGATCATGGGGTGG | 171 | 50 | GCTTGAGCTGGCATCTGTGATCCAAGCCCTGTCTTCA | chr9 | 137592962 | 137593132 |
| COL5A1 | COL5A1_12 | GCGTCCACAAGAAAAATGTCACC | GGCACAGGGGTTGGTCTG | 174 | 54 | GCGTCCACAAGAAAAATGTCACCTTGATCCTCGACTG | chr9 | 137593037 | 137593210 |
| COL5A1 | COL5A1_13 | CCATGCGAGTGCTCTGTGA | TATTCATCTGGATTGGGGTCCTG | 183 | 54 | CCATGCGAGTGCTCTGTGAGCTGCTTTTTCATGAGCG | chr9 | 137619060 | 137619242 |
| COL5A1 | COL5A1_14 | CTGCTCTTTGTCTCGGACCAC | ATGTGTCTCTTCACCAACCATCC | 188 | 53 | CTGCTCTTTGTCTCGGACCACCGGGCAGCTTATGATTA | chr9 | 137619127 | 137619314 |
| COL5A1 | COL5A1_15 | GGTTGCGGAAGGAAGGACAG | AGCTTCCACGGGCTTCTTG | 189 | 60 | GGTTGCGGAAGGAAGGACAGCAGGCTGGTCGCTCTG | chr9 | 137620438 | 137620626 |
| COL5A1 | COL5A1_16 | CTTTCAGTACACGGAAGGAGACG | CCAGCCCAACCCAGTCC | 178 | 60 | CTTTCAGTACACGGAAGGAGACGGCGAGGGTGAGAC | chr9 | 137620509 | 137620686 |
| COL5A1 | COL5A1_17 | CACTGAGATGCCTGCACCC | CACGTAGTCATAGTCCCCGATG | 197 | 63 | CACTGAGATGCCTGCACCCGGACATGCGGCAAGTCYC | chr9 | 137621984 | 137622180 |
| COL5A1 | COL5A1_18 | GACTCCAGCTGTCTCTGTCCTTG | TTCTCCTCCCCCTCGCCATA | 195 | 61 | GACTCCAGCTGTCTCTGTCCTTGGCTCCCAGGAGCTGA | chr9 | 137622051 | 137622245 |
| COL5A1 | COL5A1_19 | GACTATGACTACGTGCCCAGTGA | ACCAAACCAATGGGAAGGAAAGA | 185 | 56 | GACTATGACTACGTGCCCAGTGAGGACTACTACACGC | chr9 | 137622166 | 137622350 |
| COL5A1 | COL5A1_2 | AAGTGGTGCGGTCCCT | GCCCACAGCAGCAGCA | 198 | 79 | AAGTGGTGCGGTCCCTGCTGAGTGCGCTGCCCGGGC | chr9 | 137533925 | 137534122 |
| COL5A1 | COL5A1_20 | GCCCAGGGCCTGATGGA | ATCTCCGACGGGGAGCTG | 198 | 63 | GCCCAGGGCCTGATGGAGAGGCAGTGCCTGGTGCRT | chr9 | 137623269 | 137623466 |
| COL5A1 | COL5A1_21 | GAAGGTGCGGATGACTTGGA | AGCCCCCCAACCCCAC | 193 | 62 | GAAGGTGCGGATGACTTGGAGGGGGAGTTCACTGAC | chr9 | 137623360 | 137623552 |
| COL5A1 | COL5A1_22 | GGACTTTCTTTCTCACTTTTCTCTCT | CTGTTCACACCCTACACACCC | 198 | 55 | GGACTTTCTTTCTCACTTTTCTCTCTGATTCTCTTTCCA | chr9 | 137623857 | 137624054 |
| COL5A1 | COL5A1_23 | GAGCCAGGGCCTCTTGTG | TCTGCAAGTCACAGGATAAAGCC | 183 | 65 | GAGCCAGGGCCTCTTGTGCATGCAGCTGAAGGCCGTC | chr9 | 137630212 | 137630394 |
| COL5A1 | COL5A1_24 | GCCAGTTGGAACTTGGACCTT | ACACCTTGTGTGATCTCAGGAAA | 173 | 53 | GCCAGTTGGAACTTGGACCTTGCCCTGCGGCCCCATC | chr9 | 137630522 | 137630694 |
| COL5A1 | COL5A1_25 | CCTGGCCTGGTTGCACT | CCTCAGAGGGTCTGGTTTGGAT | 195 | 64 | CCTGGCCTGGTTGCACTCTGACTTGTCTCTCTTGGCCC | chr9 | 137642339 | 137642533 |

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|---|---|---|---|---|---|---|---|---|---|
| COL5A1 | COL5A1_26 | GGGTGCCACGTCACTGC | CTGTCCCCTTCAGGCCTCTT | 180 | 63 | GGGTGCCACGTCACTGCTCCCAGAGTGACCCTTGTCT | chr9 | 137642588 | 137642767 |
| COL5A1 | COL5A1_27 | CCACATCTCACGGCTCAGG | CCAGCTCTCAGATTTGCCAATGA | 167 | 61 | CCACATCTCACGGCTCAGGCGCCAGCAAACCGGAGC/ | chr9 | 137644353 | 137644519 |
| COL5A1 | COL5A1_28 | GAAGCCCTGTCCCCTCCC | CAGACAGCGAAGGCAAGGAT | 188 | 64 | GAAGCCCTGTCCCCTCCCCCTGCCCCTCCCCTGCCACC | chr9 | 137645591 | 137645778 |
| COL5A1 | COL5A1_29 | GACAAGGCTTTGCTCTTTCTCCT | CAAGCTGCTGTCACTAAACCACA | 165 | 61 | GACAAGGCTTTGCTCTTTCTCCTGAGAAAGGCGGACT | chr9 | 137646049 | 137646213 |
| COL5A1 | COL5A1_30 | CGCTCAACTTGGTTTAACGGAAA | GGATGACAGTGATGCCAGGG | 191 | 59 | CGCTCAACTTGGTTTAACGGAAAACCATGGCCCGGGC | chr9 | 137648520 | 137648710 |
| COL5A1 | COL5A1_31 | GGCGGCCATCACTTGGT | CCCATCGTCATGCCTGTGTC | 178 | 62 | GGCGGCCATCACTTGGTGGACACCAAGGCRGGGTGT | chr9 | 137650004 | 137650181 |
| COL5A1 | COL5A1_32 | AAAAACAAAGTGGGACCTTGGAC | TTCCTGCCCAAATCACTGAGGAG | 196 | 57 | AAAAACAAAGTGGGACCTTGGACMAGCCCTGCATGA | chr9 | 137653694 | 137653889 |
| COL5A1 | COL5A1_33 | GTGTCCAGGCTAACAGCTCATT | TAAGCTCCTGGCTGATCCCA | 198 | 58 | GTGTCCAGGCTAACAGCTCATTTCTCTAACCTTGCCTT | chr9 | 137655486 | 137655683 |
| COL5A1 | COL5A1_34 | GTGGAGTCAGGGCCAAGTG | AGACAAGCAGGGCGGTAATG | 173 | 60 | GTGGAGTCAGGGCCAAGTGGGCATAGGGGACAGAG/ | chr9 | 137657436 | 137657608 |
| COL5A1 | COL5A1_35 | AGCACTGTGAGTTCTTTCGCATT | CTGATGTGGACAGCGATGGAC | 197 | 55 | AGCACTGTGAGTTCTTTCGCATTCAGTTACATGTTTTT( | chr9 | 137658242 | 137658438 |
| COL5A1 | COL5A1_36 | GGAAGGGGATACAGTTCCCAGAG | CTCCGGACTGGAGACGTGTG | 179 | 65 | GGAAGGGGATACAGTTCCCAGAGCCCCCTTCAGTGCC | chr9 | 137658789 | 137658967 |
| COL5A1 | COL5A1_37 | CAGGGGAGGGTTCTGAGTCAAT | GATACCAGGGGTCCTCCCAG | 193 | 62 | CAGGGGAGGGTTCTGAGTCAATCAGCGCCCTCACCTT | chr9 | 137659092 | 137659284 |
| COL5A1 | COL5A1_38 | TGTGGGCAGAAATGTTGAAAAGTA | GATGAGGTGGGCAGGGCTA | 176 | 59 | TGTGGGCAGAAATGTTGAAAAGTAACCTTGGTGGCCI | chr9 | 137660158 | 137660333 |
| COL5A1 | COL5A1_39 | GAAGGGAAATGGGCTCCATGA | CACCTGGATGCTGAAGGGTAG | 194 | 57 | GAAGGGAAATGGGCTCCATGATCATGGATGCTACGC/ | chr9 | 137664529 | 137664722 |
| COL5A1 | COL5A1_4 | CTGCTGCTGCTGCTGTG | ATTCCACAGGCCAAGGAAGAAAA | 152 | 74 | ctgctgctgctgctgTGGGCGCCGCCTCCGAGCCGCGCAG | chr9 | 137534103 | 137534254 |
| COL5A1 | COL5A1_40 | CTCTGGAGTTTCCTGATGTTCCC | CAAGGCCCACAGTCCCAAC | 192 | 59 | CTCTGGAGTTTCCTGATGTTCCCCAGGCACCTCCACAC | chr9 | 137666629 | 137666820 |
| COL5A1 | COL5A1_41 | TCTAGAAAGGCTGAGACTTGTAACC | TGGTTTCATGGAAGAAGCATTGTG | 197 | 57 | TCTAGAAAGGCTGAGACTTGTAACCATTCACTCCTTTT | chr9 | 137671891 | 137672087 |
| COL5A1 | COL5A1_42 | CTGGTGCTGAGTGTGGTTGTTTG | GCCCAAATCCCAAACCTGAGATG | 177 | 56 | CTGGTGCTGAGTGTGGTTGTTTGGAGCGGGGAAGGG | chr9 | 137674418 | 137674594 |
| COL5A1 | COL5A1_43 | TCTCACCTCCTCTTTTCTGGCTT | GTCAGATCCCTCCCAAGAAAGTG | 181 | 62 | TCTCACCTCCTCTTTTCTGGCTTGCAGGGGGAGATCG( | chr9 | 137676808 | 137676988 |
| COL5A1 | COL5A1_44 | CAGAACGCATGTCCTTTCTCTCT | GACACCTAACACGGCCAGAA | 165 | 52 | CAGAACGCATGTCCTTTCTCTCTGCTCCGGGGAAACG | chr9 | 137677755 | 137677919 |
| COL5A1 | COL5A1_45 | GGCATGCAGGTGGTCCC | CCCAGGGGCCAGGCTAT | 164 | 60 | GGCATGCAGGTGGTCCCCCAGGCGGCCCATGCAGCA | chr9 | 137680914 | 137681077 |
| COL5A1 | COL5A1_46 | CAGGGCCGGGCATTTAGAG | AAGTCCCGACACACAGACAC | 198 | 61 | CAGGGCCGGGCATTTAGAGAGTGACTGAYCAGCCCC | chr9 | 137686878 | 137687075 |
| COL5A1 | COL5A1_47 | GTGTCTGTGTGTCGGGACTTG | TGTAGCCTTGCAACTTGGGTTC | 162 | 60 | GTGTCTGTGTGTCGGGACTTGAGCTGACCTTCCTTCTC | chr9 | 137687056 | 137687217 |
| COL5A1 | COL5A1_48 | CAGACGTTTTGATGACGTTGTGG | CTTGGAGACACCCCCGAAG | 167 | 54 | CAGACGTTTTGATGACGTTGTGGGCCAGAGTCTTTTC/ | chr9 | 137688132 | 137688298 |
| COL5A1 | COL5A1_49 | GGAAGAAATGACACCTGCGTTC | GCCCAGCAAGGAAGCCATTA | 187 | 58 | GGAAGAAATGACACCTGCGTTCAGAGAGCCACCGGC | chr9 | 137688586 | 137688772 |
| COL5A1 | COL5A1_50 | TTCTCAAAGGTGGTTGCTTCTCA | CGTGCAGGGTGGTCAGAG | 173 | 57 | TTCTCAAAGGTGGTTGCTTCTCAGACACGAATGAACC | chr9 | 137690192 | 137690364 |
| COL5A1 | COL5A1_51 | CAAGCGTCCTGCTGAGAACA | GTGACCCATGGAATCTGGGAAG | 170 | 65 | CAAGCGTCCTGCTGAGAACAGTGCAGGGCMGGGTG( | chr9 | 137693718 | 137693887 |
| COL5A1 | COL5A1_52 | CGTCTGTGGCTGACACTGATTTT | CTGACACAGAAGGCTCCAGAAAC | 166 | 63 | CGTCTGTGGCTGACACTGATTTTCCCCACAGGGTCCC/ | chr9 | 137694703 | 137694868 |
| COL5A1 | COL5A1_53 | CTGGTGAGAGGTCTGCGTCA | CTGCACCTGTCCCATTTCATTCC | 191 | 61 | CTGGTGAGAGGTCTGCGTCACTGGCTCCAGGAAAGC | chr9 | 137696763 | 137696953 |
| COL5A1 | COL5A1_54 | GGAATGAAATGGGACAGGTGCAG | CCTTCTGACCTGGAGAGTAGGAT | 188 | 57 | GGAATGAAATGGGACAGGTGCAGCCCTGGAGGCCTC | chr9 | 137696931 | 137697118 |
| COL5A1 | COL5A1_55 | CAGTCTGAGAGCCTTTGAAGCAG | CCCAATCCAAGGCAGTACTTACA | 176 | 61 | CAGTCTGAGAGCCTTTGAAGCAGAYTGTTTTCTTGCTC | chr9 | 137697989 | 137698164 |
| COL5A1 | COL5A1_56 | GATCTCCAGGGGAGAGAGGTC | GACAAGGCCAGACACGGAAC | 178 | 65 | GATCTCCAGGGGAGAGAGGTCCAGCTGGAGCCGCTG | chr9 | 137698036 | 137698213 |
| COL5A1 | COL5A1_57 | TGACCTGAGATCTTCTGTATTCTCT | GCCATGGGTCACTCTGGATTT | 163 | 62 | TGACCTGAGATCTTCTGTATTCTCTAGGGCGAGAAAG | chr9 | 137701002 | 137701164 |
| COL5A1 | COL5A1_58 | AAGTTTTAGGGCCACCTGGAAAG | CGCCCCCGTGCCAATA | 198 | 51 | AAGTTTTAGGGCCACCTGGAAAGGACACTGTTCTTAA | chr9 | 137701978 | 137702175 |
| COL5A1 | COL5A1_59 | CAGCCTTATCCACGATCCAAGAA | AATAACCGGCCATGGGTGAG | 198 | 59 | CAGCCTTATCCACGATCCAAGAAGCTACCTATGTCTCT | chr9 | 137703131 | 137703328 |
| COL5A1 | COL5A1_6 | GTGTTCCCAGGTGCTCCTTTC | TTTGGTGACTCTGTAAGCGACAT | 188 | 51 | GTGTTCCCAGGTGCTCCTTTCCTCTCYGTGGCTAACTC | chr9 | 137582698 | 137582885 |
| COL5A1 | COL5A1_60 | ATTGCCAGCATCCTCACCCAT | GTGTGGTGAGAACCCCACAGTTA | 173 | 64 | ATTGCCAGCATCCTCACCCATGGCCGGTTATTTCCCTG | chr9 | 137703297 | 137703469 |
| COL5A1 | COL5A1_61 | TGAAAGCTGTGTGTGTGTTTGAC | CAAATGTTTCCCCAAAACATGAGC | 188 | 52 | TGAAAGCTGTGTGTGTGTTTGACATACACATGACAGA | chr9 | 137704225 | 137704412 |
| COL5A1 | COL5A1_62 | GTACTAGCGGCTCATGTTTTGGG | GCACGAGCCTCACCTTCT | 192 | 60 | GTACTAGCGGCTCATGTTTTGGGGAAACATTTGCRTT | chr9 | 137704380 | 137704571 |

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|---|---|---|---|---|---|---|---|---|---|
| COL5A1 | COL5A1_63 | GATGGCCCACAAGGTCCC | CGTGTATGCACCCCCACAAG | 183 | 54 | GATGGCCCACAAGGTCCCCCAGGTGGAATAGGAAAC | chr9 | 137704502 | 137704684 |
| COL5A1 | COL5A1_64 | GCAGACAGCAGGCAGGATTTG | GGCCATATCCCACCCCTCC | 190 | 64 | GCAGACAGCAGGCAGGATTTGGCAAATGCTTGAAAC | chr9 | 137705732 | 137705921 |
| COL5A1 | COL5A1_65 | GTTGGCTCTGAGGACTTGACACT | GTGTGTCTGGAATACTCACAGGG | 166 | 61 | GTTGGCTCTGAGGACTTGACACTGGCCTCTTTCCTCCA | chr9 | 137706604 | 137706769 |
| COL5A1 | COL5A1_66 | CCAAAGGAGAAAGGGGAGAGAAG | GTCAGAATGATCCCAGTGCAGAG | 173 | 64 | CCAAAGGAGAAAGGGGAGAGAAGGGCGAGTCAGGC | chr9 | 137706647 | 137706819 |
| COL5A1 | COL5A1_67 | GTGTGGTCTCAGTCAGGTTGC | AACCACCAGAAAGAGGGGAAATG | 198 | 61 | GTGTGGTCTCAGTCAGGTTGCTGATGGCCTTGGCTGC | chr9 | 137707364 | 137707561 |
| COL5A1 | COL5A1_68 | TGGAGATGCATTGGGAACTGG | GGTCCCAAGAATACACTGACACC | 190 | 56 | TGGAGATGCATTGGGAACTGGTGCATGAACTCAGGG | chr9 | 137707702 | 137707891 |
| COL5A1 | COL5A1_69 | AATTGAGTCTAACGGGCCCCAA | CAAGCAAAGGTGACGGGGAG | 188 | 54 | AATTGAGTCTAACGGGCCCCAATTCCTCACACTCTGTT | chr9 | 137708817 | 137709004 |
| COL5A1 | COL5A1_7 | TCTCCTGAAGGTTCTAGATTTTCACA | ACCGCCCCAAACAGAAGG | 186 | 54 | TCTCCTGAAGGTTCTAGATTTTCACAMCTTGCCTGATC | chr9 | 137582771 | 137582956 |
| COL5A1 | COL5A1_70 | CAGGCCACACACACACACA | TCACAGCCTGGCTCCAAAAC | 180 | 63 | CAGGCCACACACACACACACCYTGAGCGCCTGCACCC | chr9 | 137709525 | 137709704 |
| COL5A1 | COL5A1_71 | GCTCCGGACCTCATTCTGC | CCCTCACAGCCTACTCACCAC | 162 | 70 | GCTCCGGACCTCATTCTGCCCTCCGCCGTCCTGCAGG | chr9 | 137710466 | 137710627 |
| COL5A1 | COL5A1_72 | GGAAGACTGGCCCCATCG | GGATCCTGGGAGACCTTGTTC | 188 | 66 | GGAAGACTGGCCCCATCGGCCCCCAGGGGGCCCCTG | chr9 | 137710530 | 137710717 |
| COL5A1 | COL5A1_73 | CCCTGTGGTGAGTAGGCTGT | CTATGCTCACCATGAGGAATGTG | 174 | 63 | CCCTGTGGTGAGTAGGCTGTGAGGGGCAGAGGGGTT | chr9 | 137710603 | 137710776 |
| COL5A1 | COL5A1_74 | CACCCAAAGCCCCAAGGATG | CGGATCAAGAGCTTGTTGAGTTT | 194 | 57 | CACCCAAAGCCCCAAGGATGAGGACTCTGATCCCCCT | chr9 | 137710795 | 137710988 |
| COL5A1 | COL5A1_75 | AATGCCCCTTCCTGTCTTCATTT | CCCAGGGATCTAAAATGCCTCTC | 197 | 60 | AATGCCCCTTCCTGTCTTCATTTTCCCACAGGGTCATC | chr9 | 137711931 | 137712127 |
| COL5A1 | COL5A1_76 | GCAGCTCCTCCTCGTCTGAA | CCACAATTCTCTAGCTCCACACT | 198 | 60 | GCAGCTCCTCCTCGTCTGAAGGTGATAACCTGCATTTT | chr9 | 137713891 | 137714088 |
| COL5A1 | COL5A1_77 | GACATGGAGCACGGTGGG | GACGGTTGTCTGGGTAGTTTGTT | 198 | 63 | GACATGGAGCACGGTGGGGCTGGAGCTGAGACCCG | chr9 | 137714776 | 137714973 |
| COL5A1 | COL5A1_78 | TCAAAGTCCCCTCATACCTCTGT | CACACACACACAGTTGCTTTCTC | 192 | 59 | TCAAAGTCCCCTCATACCTCTGTGACCAAGGGTTGATT | chr9 | 137715207 | 137715398 |
| COL5A1 | COL5A1_79 | ATATCCTGGGACCCTTCCCATC | TAGTCCACGTAGTTCTCGCCATT | 172 | 64 | ATATCCTGGGACCCTTCCCATCCTCCATCACCCACYGC | chr9 | 137716387 | 137716558 |
| COL5A1 | COL5A1_8 | GGCTGGCTTGTTTGCAGAG | GATACCCTGCTCGTTGTAGATGG | 182 | 57 | GGCTGGCTTGTTTGCAGAGAGCCATGGCTGGGTGTG | chr9 | 137591671 | 137591852 |
| COL5A1 | COL5A1_80 | CTGCCAATCCAGGCATCCAG | CCCAGGGGCCGTTTCATC | 164 | 60 | CTGCCAATCCAGGCATCCAGGACGCGGCGGAACATC | chr9 | 137716473 | 137716636 |
| COL5A1 | COL5A1_81 | CGGACGGCATGGAAGAGAT | CCATGCCCGCTTTGGG | 186 | 66 | CGGACGGCATGGAAGAGATCTTCGGCTCTCTCAACTC | chr9 | 137716561 | 137716746 |
| COL5A1 | COL5A1_82 | CTCCCTCCCCGTCTCTGAAAT | GGGCCATGGAGGGACACA | 165 | 56 | CTCCCTCCCCGTCTCTGAAATCCAGGTGAATACTGGG | chr9 | 137717613 | 137717777 |
| COL5A1 | COL5A1_83 | CTGGGGCCTTGCTCTGG | TTAAAGTGACAACCGCAAAGACG | 189 | 53 | CTGGGGCCTTGCTCTGGAGGCCGGARAARTAACCCTT | chr9 | 137721741 | 137721929 |
| COL5A1 | COL5A1_84 | CTTTGTTGCTGTGTGTGTCCC | CAGGCCACTGACTGGTAGC | 175 | 62 | CTTTGTTGCTGTGTGTGTCCCCACCCTGCTGAGCCCCA | chr9 | 137726761 | 137726935 |
| COL5A1 | COL5A1_85 | CTCTGCCCACCAGAACGTC | CGGGATACTCACAGCACAGC | 175 | 62 | CTCTGCCCACCAGAACGTCMCCTACCACTGCTACCAG | chr9 | 137726888 | 137727062 |
| COL5A1 | COL5A1_86 | GCTCCAACGACGAGGAGATG | CAGGCATCTTGGGGACAGGTAAA | 162 | 65 | GCTCCAACGACGAGGAGATGTCCTATGACAACAACCC | chr9 | 137726983 | 137727144 |
| COL5A1 | COL5A1_87 | TTTTGGAGCCAGACAGATTGTGG | CGCTTCACCGAAGTCATTGAACA | 192 | 53 | TTTTGGAGCCAGACAGATTGTGGGGGGKGATTGGTA | chr9 | 137733910 | 137734101 |
| COL5A1 | COL5A1_88 | CAGACCAAGAAAGGCTACCAGAA | GAGGTCACGAGGTTGCTCTC | 192 | 56 | CAGACCAAGAAAGGCTACCAGAAGACGGTTCTGGAG | chr9 | 137734000 | 137734191 |
| COL5A1 | COL5A1_9 | GGACTTCTCCATCCTAACAACTG | TTGCCATCTGACAGGTTGATGC | 198 | 59 | GGACTTCTCCATCCTAACAACTGTGAAAGCCAAGAAA | chr9 | 137591771 | 137591968 |
| COL5A2 | COL5A2_1 | ACTTCAAGAGTCTCAGGATCAACT | GCACGCTTGCCCATCATAGA | 192 | 46 | ACTTCAAGAGTCTCAGGATCAACTTCAAACAGTCAAA | chr2 | 189898697 | 189898888 |
| COL5A2 | COL5A2_10 | CGTTTTGTTTTTGTCATCAGGAGC | ACAATGTGTTAAATGTCTTTCCAATCT | 198 | 51 | CGTTTTGTTTTTGTCATCAGGAGCCGCCTGATCTTCAG | chr2 | 189904131 | 189904328 |
| COL5A2 | COL5A2_11 | TTGGACGGAATCTGAGCTATTGA | ACAGTCTTTGTTTCTTGCAGGGT | 191 | 49 | TTGGACGGAATCTGAGCTATTGAATAAATAGCATTTC | chr2 | 189906249 | 189906439 |
| COL5A2 | COL5A2_12 | CTCGTACACCTGGAGGTCCAAT | TCTTAGAAATCACTGTTACAGCTCCATA | 193 | 42 | CTCGTACACCTGGAGGTCCAATTGGCCCAAGTGGCCC | chr2 | 189906338 | 189906530 |
| COL5A2 | COL5A2_13 | ACCAGGAAAACGATACTCAAGCA | TGGCACAATGCAGGATCCAAATA | 198 | 39 | ACCAGGAAAACGATACTCAAGCATTAGCAGTACATCA | chr2 | 189907359 | 189907556 |
| COL5A2 | COL5A2_14 | ACATATCCACCTATTTTACAGACAGAT | TGGTGACAAAGGTGATCATGGAG | 188 | 44 | ACATATCCACCTATTTTACAGACAGATAAATGTTCRTG | chr2 | 189907780 | 189907967 |
| COL5A2 | COL5A2_15 | GGGCAGAATAATACTTAAAGGAATAACTTACA | TCATGCCATATCTCTATTTCTAGGGAC | 162 | 50 | GGGCAGAATAATACTTAAAGGAATAACTTACAGGAG | chr2 | 189907846 | 189908007 |
| COL5A2 | COL5A2_16 | ATAACTTACAGGAGGGCCAGGA | AAATTTTAGTCTCAACAATAATATGTAGCAAG | 178 | 46 | ATAACTTACAGGAGGGCCAGGAAGACCCTGAAGACC | chr2 | 189907868 | 189908045 |
| COL5A2 | COL5A2_17 | AGCTTGAggaATTTCAtATTTTTCAGTTAT | TTTCTTTTAGGGTTCTCGGGGTC | 172 | 33 | AGCTTGAggaATTTCAtATTTTTCAGTTATGAATCTTAA | chr2 | 189909797 | 189909968 |
| COL5A2 | COL5A2_18 | AGAGAACTTACAGGTAATCCACGTT | ACGTATTGTTGACATCCTGTATCTATG | 148 | 37 | AGAGAACTTACAGGTAATCCACGTTTCCnnGCTCGAC | chr2 | 189909894 | 189910041 |

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|---|---|---|---|---|---|---|---|---|---|
| COL5A2 | COL5A2_2 | ATTTCAACGCCGAATTCCTGGTC | AGGTTGCTGTCTAACATACTTGGA | 193 | 41 | ATTTCAACGCCGAATTCCTGGTCTGWGCCRCMAACA | chr2 | 189898818 | 189899010 |
| COL5A2 | COL5A2_20 | GCATATGGGTGTGCAAAACTGTC | ATCATGGTTATTCTTGTTAGGGTGA | 176 | 56 | GCATATGGGTGTGCAAAACTGTCAGTGTGAAATTGAC | chr2 | 189910478 | 189910653 |
| COL5A2 | COL5A2_21 | TTACCGGATCTCCTCTTTGTCCT | ACATGAACATATGGAATATTGTTGTTTTAGA | 182 | 47 | TTACCGGATCTCCTCTTTGTCCTGCATCTCCTGGAGCA | chr2 | 189910522 | 189910703 |
| COL5A2 | COL5A2_22 | AATTAAAAAGATTTCAGATTTGCATGACTT | TGCTGTCATTTTTTGACAATTGGA | 196 | 35 | AATTAAAAAGATTTCAGATTTGCATGACTTTAGATTTT | chr2 | 189912874 | 189913069 |
| COL5A2 | COL5A2_23 | GACACCAGATAACAAGAGAAGAGT | TCAATTTCTTCACAAGTGTTTGACAT | 196 | 45 | GACACCAGATAACAAGAGAAGAGTTATTTTCACTGTA | chr2 | 189914028 | 189914223 |
| COL5A2 | COL5A2_24 | AGAGACTCAAAAATTAATGTCCCTACA | GCAACGTGGAGAGAGAGGC | 173 | 39 | AGAGACTCAAAAATTAATGTCCCTACAATACTGTTTAA | chr2 | 189915165 | 189915337 |
| COL5A2 | COL5A2_25 | GACCGATGCAGCTACTCACC | GGTACAGTTTTACCCTGGATAGTT | 179 | 57 | GACCGATGCAGCTACTCACCGCTGGGCCTGGTAGGCC | chr2 | 189915276 | 189915454 |
| COL5A2 | COL5A2_26 | TTGTGACACTGATCATTATGGGTT | GGGGACCCTGGCTCTCAT | 178 | 54 | TTGTGACACTGATCATTATGGGTTTCTATTTGTAAATA | chr2 | 189915967 | 189916144 |
| COL5A2 | COL5A2_27 | TACAGGTTGCCCATCTTCTCCT | CCCTCCTTGGTGTTTCTTTCTTTG | 198 | 62 | TACAGGTTGCCCATCTTCTCCTGGGTCCCCTTTGTCTC | chr2 | 189916043 | 189916240 |
| COL5A2 | COL5A2_28 | TGTGTAATTATTTCATTATCAGTGACTTGTCT | AAGGCTTCAGTCTTCCTGTGAAA | 198 | 38 | TGTGTAATTATTTCATTATCAGTGACTTGTCTCACTAA | chr2 | 189916850 | 189917047 |
| COL5A2 | COL5A2_29 | ACATGACCAGGAAGCACTAGGTA | ACATTCAGCCTCTTTTGCTTCAC | 176 | 43 | ACATGACCAGGAAGCACTAGGTAACTAKAATTAGCTG | chr2 | 189917406 | 189917581 |
| COL5A2 | COL5A2_3 | AAGGTAAAATTGCCCCCAGTTCT | CCTCAAAAAAGCTGTGGTTCTCA | 198 | 34 | AAGGTAAAATTGCCCCCAGTTCTAGTGCYRTAATAGT | chr2 | 189899544 | 189899741 |
| COL5A2 | COL5A2_32 | CTCCAAACATGGGGCACTTGA | GCTTGTTTGTATAATTTTTTATAGGGTCCTGA | 184 | 47 | CTCCAAACATGGGGCACTTGACTCAAGTTATGYCTTTT | chr2 | 189917585 | 189917768 |
| COL5A2 | COL5A2_34 | AGATAAGTGTTTATTTGTAAATTAGGGATATTTGA | TCTTTGTCTCCTCCTAGGGTTCT | 115 | 42 | AGATAAGTGTTTATTTGTAAATTAGGGATATTTGAAA | chr2 | 189918106 | 189918220 |
| COL5A2 | COL5A2_35 | AAATTATACCTGGGGTCCGGCAA | AGGATAATGTGTGAAAGCTACAGTAATC | 106 | 46 | AAATTATACCTGGGGTCCGGCAAAACCAACAGCTCCA | chr2 | 189918141 | 189918246 |
| COL5A2 | COL5A2_36 | ACATAACCTAAAACCAATAAGCATTGT | TGGACAGTAACCATCTAAAATCTGC | 195 | 37 | ACATAACCTAAAACCAATAAGCATTGTTTTATATAAAT | chr2 | 189918512 | 189918706 |
| COL5A2 | COL5A2_37 | TGTTATAAAATGAAAAGATTTATGAAAGAGCC | ACCTCAATATGCCTATGTTCTGTT | 172 | 41 | TGTTATAAAATGAAAAGATTTATGAAAGAGCCTGCTA | chr2 | 189918800 | 189918971 |
| COL5A2 | COL5A2_38 | CCAACTCCTGACTACCAAGGAAA | GTGGCATAGGAGAAAAAGGTGCT | 170 | 43 | CCAACTCCTGACTACCAAGGAAACATGACTGACTTTA | chr2 | 189921582 | 189921751 |
| COL5A2 | COL5A2_39 | CCTAGCCCAGCTAGAAAAGGAAT | TGACAATTAGCCTTCACTCTCAT | 180 | 41 | CCTAGCCCAGCTAGAAAAGGAATACTTTCACTTACTCT | chr2 | 189921664 | 189921843 |
| COL5A2 | COL5A2_4 | AGCAAGTGTCTTGAAGAACGATA | CTCAGATGACTTTTTTGCGCCTT | 198 | 39 | AGCAAGTGTCTTGAAGAACGATATACCGGAATCTAAT | chr2 | 189899644 | 189899841 |
| COL5A2 | COL5A2_40 | TCAGCAGAAAGTCTGAATAAATGAAC | TGGTATGGTCACTTAATGTTGGT | 197 | 45 | TCAGCAGAAAGTCTGAATAAATGAACTGnnaaaaaaaa | chr2 | 189921989 | 189922185 |
| COL5A2 | COL5A2_41 | TCTCACACCATCATGCGTTTATT | GTGCTAGGGAGAACGAGGAAATC | 180 | 46 | TCTCACACCATCATGCGTTTATTRAGCAGTAATTTTAA | chr2 | 189923081 | 189923260 |
| COL5A2 | COL5A2_42 | ATGACACTTACTTTTGGGCCATC | TTCCGCAGTAGAAGCCATTTCTC | 198 | 44 | ATGACACTTACTTTTGGGCCATCAGGACCATGTCCTCC | chr2 | 189923144 | 189923341 |
| COL5A2 | COL5A2_43 | TTAAAACTGAAGCCAGTGGGAAA | AAACTAGGTGTATGAACTGGAAAGT | 186 | 36 | TTAAAACTGAAGCCAGTGGGAAACAAnnTTAATCATG | chr2 | 189923521 | 189923706 |
| COL5A2 | COL5A2_44 | AAAGCACAACAGAGCCTCACA | CACAGATTCACAATTTTATTTTCTTACTTTTG | 177 | 39 | aaagcacaacagagcctcacacataaaaagtgATAATTGAGCC | chr2 | 189925371 | 189925547 |
| COL5A2 | COL5A2_45 | TGTAGAATTTCAAATCTTCTGACCATATC | GATCTGGTTATATTCACAATTATTTTCTCCT | 193 | 35 | TGTAGAATTTCAAATCTTCTGACCATATCYTTTTTTTTW | chr2 | 189926191 | 189926383 |
| COL5A2 | COL5A2_46 | TCCCATACATTCTTATTCACTTTCCC | ATCTGTGTGTGATACTAGGGAGC | 193 | 40 | TCCCATACATTCTTATTCACTTTCCCTGAAACTTACSCA | chr2 | 189927470 | 189927662 |
| COL5A2 | COL5A2_47 | CAGGACCAGAAGGACCAACTTC | GGAAACCTGGAGAAGCAGGAAA | 178 | 40 | CAGGACCAGAAGGACCAACTTCACCATCTTTTCCAGG | chr2 | 189927602 | 189927779 |
| COL5A2 | COL5A2_48 | GAGCTCCCTAGTATCACACACAG | GGAATTATACAAAAGTTTCATTTATTCTTTAGGG | 184 | 37 | GAGCTCCCTAGTATCACACACAGATATTTGTGAGGTG | chr2 | 189927638 | 189927821 |
| COL5A2 | COL5A2_49 | ATTTCCTGCTTCTCCAGGTTTCC | CTTCCAGGCCCCAAAGGTAG | 165 | 41 | ATTTCCTGCTTCTCCAGGTTTCCCAGGGTCACCCTAAA | chr2 | 189927757 | 189927921 |
| COL5A2 | COL5A2_5 | GAGGTTCTTAGCTTGATCGTCCA | GGCATTATGAAACCCTTCAGTCTT | 198 | 39 | GAGGTTCTTAGCTTGATCGTCCATGTATCCTACACTGT | chr2 | 189899738 | 189899935 |
| COL5A2 | COL5A2_50 | TGTCAAAAACATACCTCCTCCAA | ACTTACATGGCTCCTGTCAATTC | 196 | 53 | TGTCAAAAACATACCTCCTCCAAATGAGGATCATGAT | chr2 | 189927829 | 189928024 |
| COL5A2 | COL5A2_51 | TCATTTAAGTTGCATGTCTGTTGAAAAA | ACTGCATATCAGCAACAAACTGAC | 162 | 36 | TCATTTAAGTTGCATGTCTGTTGAAAAATATTAGTGGT | chr2 | 189928642 | 189928803 |
| COL5A2 | COL5A2_52 | CACTTCTCCCCTTTGATGTAGCA | TTTCTTCATGCATCTGCTTTGCC | 174 | 53 | CACTTCTCCCCTTTGATGTAGCAAACACTTGCTATATT | chr2 | 189929240 | 189929413 |
| COL5A2 | COL5A2_53 | CATGCAGGCCATAGCTAGATCA | ACAACAATTAAGAATCACATTTTGGTCAT | 180 | 48 | CATGCAGGCCATAGCTAGATCACCGTGCTGAAAAATG | chr2 | 189929639 | 189929818 |
| COL5A2 | COL5A2_54 | TCCCTCACAACTGTAAGAATGTGTT | GGTTGGATGGGTCTTTCTGGTAA | 194 | 49 | TCCCTCACAACTGTAAGAATGTGTTGTATTATTTAAAT | chr2 | 189931074 | 189931267 |
| COL5A2 | COL5A2_55 | TTTGAGCTGTACACTTCCAGACA | TGGACTAGCTAAATGTCCTGGTTC | 168 | 38 | TTTGAGCTGTACACTTCCAGACAATACTATGTTCTACT | chr2 | 189931392 | 189931559 |
| COL5A2 | COL5A2_56 | ACTCTTGGCCCTCGTAGTTAGAT | ACTTACCACATCACTCTTGCTGTT | 189 | 51 | ACTCTTGGCCCTCGTAGTTAGATTACACTAAAGGATG | chr2 | 189932681 | 189932869 |
| COL5A2 | COL5A2_57 | GCCAATGTCTAAAGAATCATGCC | TCCTTTTTGAAGATGGCTGGACA | 198 | 39 | GCCAATGTCTAAAGAATCATGCCCATTTGAGCTTCAC | chr2 | 189932893 | 189933090 |

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|---|---|---|---|---|---|---|---|---|---|
| COL5A2 | COL5A2_58 | CAGCTTTCTGGGCTGGTTCTTA | TGTACAATGCCACTCTCGTATTT | 197 | 51 | CAGCTTTCTGGGCTGGTTCTTAAATATGCTAGAAACTT | chr2 | 189933472 | 189933668 |
| COL5A2 | COL5A2_59 | TCATTCTTCACTTTGGGACTCATGT | TGAATACATGTCTGATTACTTTTCTGGT | 163 | 36 | TCATTCTTCACTTTGGGACTCATGTAATCATGTAGCGT | chr2 | 189936697 | 189936859 |
| COL5A2 | COL5A2_6 | AGCAAAGTCCTAAATAAATCAAAAATATGTAATAA | CCCATCCAGTGTACCACGTAAAA | 176 | 33 | AGCAAAGTCCTAAATAAATCAAAAATATGTAATAART | chr2 | 189901260 | 189901435 |
| COL5A2 | COL5A2_60 | tgtacaaatGGAAGAATGCATGAATAA | AGGCAAATAAGAGAAAATATAGTCTAAAATGTAA | 175 | 32 | tgtacaaatGGAAGAATGCATGAATAAATTAATGAATTA | chr2 | 189940058 | 189940232 |
| COL5A2 | COL5A2_61 | TTCAGTAAACCAAATCTGAAAATGAATTG | TCAAATTAGGTGCTTCAAGAGACATT | 171 | 42 | TTCAGTAAACCAAATCTGAAAATGAATTGAAATACAC | chr2 | 189943170 | 189943340 |
| COL5A2 | COL5A2_62 | TCTTGTTGTAATCTAAAAGGCAAGGA | ACACAGAACAAAGTGATGTATCGG | 182 | 40 | TCTTGTTGTAATCTAAAAGGCAAGGAAATATAACCTT | chr2 | 189943719 | 189943900 |
| COL5A2 | COL5A2_63 | ACATTTGAAGCAAAACTAAGATGCC | TGGTTCTTATGCCTTTGAGGATTGA | 181 | 36 | ACATTTGAAGCAAAACTAAGATGCCRAAGTGAGGTTA | chr2 | 189944644 | 189944824 |
| COL5A2 | COL5A2_64 | TGCAACCATAGACAGTTAAGGACA | TGGATTTCCTGGGGCTCCT | 168 | 43 | TGCAACCATAGACAGTTAAGGACAATTGACAARTTGA | chr2 | 189945594 | 189945761 |
| COL5A2 | COL5A2_65 | GAACTTACTCGGTGACCCTTCAG | TCTTAATATGTTGCTGGAAAACTGTG | 180 | 41 | GAACTTACTCGGTGACCCTTCAGACCTGGAAGACCAG | chr2 | 189945708 | 189945887 |
| COL5A2 | COL5A2_66 | TGTCTCCATTTACTTAGTGCCTGA | TTTTGCCTTCCCAATCTCCTACA | 198 | 36 | TGTCTCCATTTACTTAGTGCCTGATACATGTGCATACA | chr2 | 189948604 | 189948801 |
| COL5A2 | COL5A2_67 | CCTGAATGGAAAATGAGGAAAGG | TTGACATTTCATTTGTCTCAATAATGTTTT | 180 | 38 | CCTGAATGGAAAATGAGGAAAGGTAGCTTACATCTTC | chr2 | 189949855 | 189950034 |
| COL5A2 | COL5A2_68 | GGACCTGGGAAGATAAATAACTCAATA | GGGTTTAATATTCTATTTTTCCTTGGTTTG | 200 | 40 | GGACCTGGGAAGATAAATAACTCAATATTTGACATCA | chr2 | 189950355 | 189950554 |
| COL5A2 | COL5A2_69 | TTAAAACCAGCCAAAAGCAGTCA | TGCAACGTTTCTCCTCATTTGTT | 175 | 39 | TTAAAACCAGCCAAAAGCAGTCATGTCACAGAGACCT | chr2 | 189951351 | 189951525 |
| COL5A2 | COL5A2_7 | GGAGATTTACTGGCCCACC | GACTTATAGTCATGATTGAGATTGTCTTT | 198 | 36 | GGAGATTTACTGGCCCACCAGGTTTTACGTGGTACAC | chr2 | 189901391 | 189901588 |
| COL5A2 | COL5A2_71 | tgtaCgACTGTGTTTAAGAAGATGC | TTCAGCTCAAATGGCTGGGT | 190 | 35 | tgtaCgACTGTGTTTAAGAAGATGCATGTTATTCTTTGA | chr2 | 189953304 | 189953493 |
| COL5A2 | COL5A2_72 | CAGTAAAATTTATGCTTACCACAGAGCC | CATTTATCCATATGAAAAGGAcGTTGATGTAT | 171 | 39 | CAGTAAAATTTATGCTTACCACAGAGCCAGGCATTAG | chr2 | 189953402 | 189953572 |
| COL5A2 | COL5A2_74 | ACGTGACATCAAACAATGCACAC | TTTAACTGGCTTGTTTTCCAGGG | 162 | 56 | ACGTGACATCAAACAATGCACACAACTCACCCTGCTC | chr2 | 189957006 | 189957167 |
| COL5A2 | COL5A2_75 | CTGCTCAAGCCATCGGGTC | CCTTGCCATTAAGAAGTCTGTGC | 197 | 51 | CTGCTCAAGCCATCGGGTCCTGGGTGGGACGGATGT | chr2 | 189957037 | 189957233 |
| COL5A2 | COL5A2_76 | TGGAGGTGAAAGAGGAATAGTGC | TTTTCTGTTTTAGGGACCTCCAG | 174 | 51 | TGGAGGTGAAAGAGGAATAGTGCTCCCAGCTTCTTGC | chr2 | 189961896 | 189962069 |
| COL5A2 | COL5A2_77 | CAACTTACAGGTCTTCCTTTTGGC | AGTGTGGTATTTCTGTTTTCCAATTTT | 167 | 37 | CAACTTACAGGTCTTCCTTTTGGCCCTCGCTCTCCTCTT | chr2 | 189961995 | 189962161 |
| COL5A2 | COL5A2_78 | AGAGACCAAGTATCATTGTTTAATTCTTT | GCAGAAACTTTACCTTTACAAATTTTCTTGTT | 191 | 34 | AGAGACCAAGTATCATTGTTTAATTCTTTTATCTTCTCA | chr2 | 189963337 | 189963527 |
| COL5A2 | COL5A2_79 | GCTAAGTTTATTTAAGGTACAAGGAAACA | ACATGGCATATTCTAGGGTGACAT | 170 | 35 | GCTAAGTTTATTTAAGGTACAAGGAAACAATGATTAT | chr2 | 189964784 | 189964953 |
| COL5A2 | COL5A2_8 | tggaatgCAGTTGAGAATAAACAATC | ACCCAGGGGTTCATGCT | 200 | 50 | tggaatgCAGTTGAGAATAAACAATCAGAAAMAACGG | chr2 | 189903930 | 189904129 |
| COL5A2 | COL5A2_80 | TGTGTGGATAGTATTGGATATAAGTCTGC | ACTGTAATTCTGACTCCAGAAGAAATC | 185 | 29 | TGTGTGGATAGTATTGGATATAAGTCTGCTTATGAAA | chr2 | 189968927 | 189969111 |
| COL5A2 | COL5A2_81 | TGAGTTGCTGAATGCTGAAAGTG | AAGATAGAATGCCAGGATGTGCT | 194 | 45 | TGAGTTGCTGAATGCTGAAAGTGAAAAACACTGCAAC | chr2 | 189974863 | 189975056 |
| COL5A2 | COL5A2_82 | TTGTGAACAGACAGGACAGCATT | TGGCCAGATGTACTTAAACAGGG | 163 | 52 | TTGTGAACAGACAGGACAGCATTCCCCAGGGGGCGT | chr2 | 189974979 | 189975141 |
| COL5A2 | COL5A2_83 | ATCTTGTCACAGAGAATGGCTCC | TGGCTCACCTTTTATTTTCTCAATTCT | 194 | 39 | ATCTTGTCACAGAGAATGGCTCCRTTGTCACAGACAC | chr2 | 189975052 | 189975245 |
| COL5A2 | COL5A2_84 | ACCTATTTCCCAAACCGTGCAAT | TTTTCACTCTCAGGAGAACCCAC | 193 | 41 | ACCTATTTCCCAAACCGTGCAATAAACACTACAAGCA | chr2 | 190044178 | 190044370 |
| COL5A2 | COL5A2_9 | CTGGGTGCTTTTTCGAGCCATC | CTTGGGGATATCATGGGGCACTA | 181 | 51 | CTGGGTGCTTTTTCGAGCCATCGGGGCTGCGCATGGT | chr2 | 189904046 | 189904226 |

Genomic co-ordinates based on GRCh37/hg19 human reference sequence

**Table S2** Oligonucleotide sequences of Aortopathy NGS panel

| Gene | Assay_Name | Forward Primer | Reverse Primer | Length | % GC | Amplicon | Chr | From | To |
|---|---|---|---|---|---|---|---|---|---|
| ACTA2 | ACTA2_1 | TGAAGGCATAATTCCACAGGACA | GCAAATACTCTGTCTGGATCGGT | 191 | 49 | TGAAGGCATAATTCCACAGGACATTCACAGTTGTGTC | chr10 | 90694914 | 90695104 |
| ACTA2 | ACTA2_2 | GGCCCGGCTTCATCGTAT | AACATCCAGGCTCTGTCCTACC | 198 | 50 | GGCCCGGCTTCATCGTATTCCTGTTTGCTGATYCACAT | chr10 | 90695008 | 90695205 |
| ACTA2 | ACTA2_3 | TCTGTGGTTATAGGGCTGACACT | GACATCAGGAAGGACCTCTATGC | 185 | 54 | TCTGTGGTTATAGGGCTGACACTGCTGGCGGCATTG( | chr10 | 90697756 | 90697940 |
| ACTA2 | ACTA2_4 | CATGGTGCTGGGTGCTAGG | ACCATGGCCTGTGTCTCTTTT | 198 | 52 | CATGGTGCTGGGTGCTAGGGCCGYGATCTCMTTCTG | chr10 | 90697827 | 90698024 |
| ACTA2 | ACTA2_5 | GCTGGCTTGATATGGAAGAAGACA | ACTGCCGCATCCTCATCCT | 181 | 53 | GCTGGCTTGATATGGAAGAAGACAATGACTCCCCTTC( | chr10 | 90699201 | 90699381 |
| ACTA2 | ACTA2_6 | TTTGTTGCCTACCGATGAAGGAT | CGGGACATCAAGGAGAAACTGTG | 187 | 51 | TTTGTTGCCTACCGATGAAGGATGGCTGGAACAGGG | chr10 | 90699252 | 90699438 |
| ACTA2 | ACTA2_7 | CCATCAGGCAACTCGTAACTCTT | CACCTGTGCAGACCCTAATGTTT | 174 | 49 | CCATCAGGCAACTCGTAACTCTTCTCAAGGGAGGATC | chr10 | 90699332 | 90699505 |
| ACTA2 | ACTA2_8 | AGTGAGGATGGTCCTGGAAGTTA | CCATCTATGAGGGCTATGCCTTG | 192 | 55 | AGTGAGGATGGTCCTGGAAGTTACTGAGCAACACAC | chr10 | 90700914 | 90701105 |
| ACTA2 | ACTA2_9 | TCAGGATCTTCATGAGGTAGTCAG | ACTTGTCCAGCAAGTAACCACAT | 197 | 54 | TCAGGATCTTCATGAGGTAGTCAGTGAGATCTCGGC( | chr10 | 90701016 | 90701212 |
| ACTA2 | ACTA2_10 | CTCCAACCAGCTTGCTGTCC | TGCTCTCCTGACCATTCTTTGTC | 187 | 52 | CTCCAACCAGCTTGCTGTCCCGCCCAGCCACCTACCA( | chr10 | 90701507 | 90701693 |
| ACTA2 | ACTA2_11 | CTAACAGAAGTTTCCCCAGACCC | CTCTGTCCCCCAACTCACTAGAT | 187 | 55 | CTAACAGAAGTTTCCCCAGACCCCASAGTGTTGTGTG | chr10 | 90703499 | 90703685 |
| ACTA2 | ACTA2_12 | ACTTGAGTCATTTTCTCCCGGTT | AGTAGCTTCTGGTCCCTTTTTGG | 197 | 53 | ACTTGAGTCATTTTCTCCCGGTTGGCCTTGGGGTTCA( | chr10 | 90703552 | 90703748 |
| ACTA2 | ACTA2_13 | AGTTGAGCAATGTGAGCCAGTTA | TGACGAAGCACAGAGCAAAAGAG | 198 | 49 | AGTTGAGCAATGTGAGCCAGTTATTTCCCCAGCAGTA | chr10 | 90706905 | 90707102 |
| ACTA2 | ACTA2_14 | CATACCTTTTCCATGTCGTCCCA | ACAAGTTTTGGGAGATGCTGACT | 180 | 47 | CATACCTTTTCCATGTCGTCCCAGTTGGTGATGATGC( | chr10 | 90707010 | 90707189 |
| ACTA2 | ACTA2_15 | TGGGGATAAACATGAACACAGAGG | ATGTGTGAAGAAGAGGACAGCAC | 198 | 51 | TGGGGATAAACATGAACACAGAGGAACCTAATCTGT | chr10 | 90708490 | 90708687 |
| ACTA2 | ACTA2_16 | CCACAATGGATGGGAAAACAGC | GTGCCACAAATGCCCAATTACAG | 188 | 54 | CCACAATGGATGGGAAAACAGCCCTGGGAGCATCGT | chr10 | 90708576 | 90708763 |
| FBN1 | FBN1_1 | TGTTTTTCTTTTAATTATTTGGTCTCTGGA | CCAGTGGCTGGAACCTATTCAT | 190 | 34 | TGTTTTTCTTTTAATTATTTGGTCTCTGGATGGTGAAT | chr15 | 48703150 | 48703339 |
| FBN1 | FBN1_2 | TCATCTTCAGATTATCACCCAGTTC | ACCAAAAGGAAGGGATCAGCTAC | 174 | 39 | TCATCTTCAGATTATCACCCAGTTCACCACTKAGGTAC | chr15 | 48703210 | 48703383 |
| FBN1 | FBN1_3 | GCCACTGGCTTCTTCTTTGTGAA | AGACAGCCATCTTTGCTTTCAAT | 193 | 42 | GCCACTGGCTTCTTCTTTGTGAAGTGGAGGTAGCTGA | chr15 | 48703332 | 48703524 |
| FBN1 | FBN1_4 | GAACCTTGTTACTGACGTGGGAA | TTAGTGTGAAATTTGAGTCATTTTTTCTTT | 191 | 38 | GAACCTTGTTACTGACGTGGGAAATATTGAAAGCAA, | chr15 | 48703477 | 48703667 |
| FBN1 | FBN1_5 | CTTGGAGGAAACCACAGGAATCT | GGATGACAATTCACTCTCCCCAG | 187 | 50 | CTTGGAGGAAACCACAGGAATCTGGAAGGGCTTTCC | chr15 | 48704691 | 48704877 |
| FBN1 | FBN1_6 | GCATCAGTTTCGTTTGTGCTTCT | CAGGCACTGTGTTTCTGGAATG | 165 | 52 | GCATCAGTTTCGTTTGTGCTTCTCCGTTTCCTGCCCCY | chr15 | 48704779 | 48704943 |
| FBN1 | FBN1_7 | CTGGGGAGAGTGAATTGTCATCC | ATCTCACAACTGCAAGGAACAGG | 186 | 50 | CTGGGGAGAGTGAATTGTCATCCATTTCACCACTGAC( | chr15 | 48704855 | 48705040 |
| FBN1 | FBN1_8 | TGCTAGGACAGGTAATTTTGAGTT | AGACATCAATGAATGTGGCTCTG | 200 | 49 | TGCTAGGACAGGTAATTTTGAGTTCAGTATACTTAAT | chr15 | 48707644 | 48707843 |
| FBN1 | FBN1_9 | AATCTCCAACCATGACCAGGAAG | GCCGGCTTCCAGTATGAACAG | 184 | 55 | AATCTCCAACCATGACCAGGAAGAGCACTGCTTACCC | chr15 | 48707698 | 48707881 |
| FBN1 | FBN1_10 | TCATTGATGTCTTGGCATCCTCC | CCTCAATAGAAATCTCTGGCTGCT | 189 | 52 | TCATTGATGTCTTGGCATCCTCCACTGAACTGTTCATA | chr15 | 48707832 | 48708020 |
| FBN1 | FBN1_11 | TTGCTTCATAGGACCTGATAGCC | TTCTTTTTCAGACGTGGACGAGT | 186 | 53 | TTGCTTCATAGGACCTGATAGCCATGCATCTTGAGAG | chr15 | 48712829 | 48713014 |
| FBN1 | FBN1_12 | CTGTAGCCCCCAATGATGTTCTG | GTAGGATGTGTAGGGGCCAGATT | 162 | 51 | CTGTAGCCCCCAATGATGTTCTGGCAGCCATGCTGGC | chr15 | 48712937 | 48713098 |
| FBN1 | FBN1_13 | GGCTGATGATGAAGGTGCCAATA | GACATCAATCTGTGCGGGTCTAA | 193 | 54 | GGCTGATGATGAAGGTGCCAATAGCCACACAGGCCA | chr15 | 48713671 | 48713863 |
| FBN1 | FBN1_14 | CCGGTCTGATCAAGTGAGAATCC | AGAGCTTTGGGGAATTTTAACCC | 164 | 49 | CCGGTCTGATCAAGTGAGAATCCCCGCTGGCATTCAC | chr15 | 48713769 | 48713932 |
| FBN1 | FBN1_15 | TCCCAACAGCAGAGGAAATAGAA | GATGAGTGTGCAACCAAGCAAC | 193 | 44 | TCCCAACAGCAGAGGAAATAGAAAATAATCCCTTAA/ | chr15 | 48714068 | 48714260 |
| FBN1 | FBN1_16 | CAGGACGTATGGTGTTGGGTAAA | CCTGATCCTGTTTTGTTGGCTTG | 166 | 46 | CAGGACGTATGGTGTTGGGTAAATCYGGGAGGACAT | chr15 | 48714154 | 48714319 |
| FBN1 | FBN1_17 | GTGGAGTTCTTACAGGCAAAGGA | GCTCCCAAACCCTGCAATTTTATC | 179 | 48 | GTGGAGTTCTTACAGGCAAAGGAATGCAGCCATGTG | chr15 | 48717490 | 48717668 |
| FBN1 | FBN1_18 | TGAGGGGCAATGGTCAATTCTAC | ATGCACAGTCACGCTGTATTTCT | 184 | 46 | TGAGGGGCAATGGTCAATTCTACTTTACCTTTGCAGC | chr15 | 48717538 | 48717721 |
| FBN1 | FBN1_19 | TCCTATGAAACTGCACAGACTTTTT | GCCGAAATGGGGAATGTGTCAA | 198 | 37 | TCCTATGAAACTGCACAGACTTTTTAGATTTTTAGCTT | chr15 | 48717831 | 48718028 |
| FBN1 | FBN1_20 | CCACTTGAGGATAAGCCATCAGAAA | ACAGATATCGATGAATGCAAGGTT | 166 | 41 | CCACTTGAGGATAAGCCATCAGAAATAGACACTTACC( | chr15 | 48717900 | 48718065 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| FBN1 | FBN1_21 | CATTGACACATTCCCCATTTCGG | TCTTAGGCCCAAAATATAGTAACACA | 174 | 30 | CATTGACACATTCCCCATTTCGGCAAACATCGTGAAT | chr15 | 48718005 | 48718178 |
| FBN1 | FBN1_22 | TCACACAAAAAACAAATAAATAGATTCCC | CACCAAATCGGAATGCTGCTG | 191 | 48 | TCACACAAAAAACAAATAAATAGATTCCCTGCAAGTA | chr15 | 48719704 | 48719894 |
| FBN1 | FBN1_23 | GAGTTTCTTGAAAGCCACAGTCC | CCCCTTTGCCATATAATGTCCCT | 198 | 54 | GAGTTTCTTGAAAGCCACAGTCCCCTGGAAAGGGCA | chr15 | 48719801 | 48719998 |
| FBN1 | FBN1_24 | AGAAGTCTGGGTTTCCAGCATCC | CCAGGGATCTGTGAGAATGGG | 173 | 57 | AGAAGTCTGGGTTTCCAGCATCCCAGTGTGGAGGCT | chr15 | 48720473 | 48720645 |
| FBN1 | FBN1_25 | TGCCAACTGTACTCACCAAGG | TGGTCAGATGACTCTTCTTGTTT | 190 | 49 | TGCCAACTGTACTCACCAAGGCACTCSTCCTGGTTGG | chr15 | 48720527 | 48720716 |
| FBN1 | FBN1_26 | GTTCCTTCTGTCCACTGTCACTT | GTGTGAAGAGGGAAAACATGACT | 184 | 47 | GTTCCTTCTGTCCACTGTCACTTCTGATGCACTCAAAG | chr15 | 48722806 | 48722989 |
| FBN1 | FBN1_27 | GTGCCAATGAGGTTCTTGCATTC | CAGCCAGTAGTGAAATAACAGATGA | 197 | 33 | GTGCCAATGAGGTTCTTGCATTCCATTTGTTTTTCAGT | chr15 | 48722927 | 48723123 |
| FBN1 | FBN1_28 | CTCCCCTCACAGATAAAGCTTCC | AATGAATGTGCCCAGAATCCTCT | 173 | 48 | CTCCCCTCACAGATAAAGCTTCCTGGCTTAGATGACC | chr15 | 48725008 | 48725180 |
| FBN1 | FBN1_29 | TGACTCACCTTTGCACATCCTAC | TTGGTAGGTTCCCTTTTGTTGCT | 193 | 46 | TGACTCACCTTTGCACATCCTACGGTCTTCTCTGAGCA | chr15 | 48725055 | 48725247 |
| FBN1 | FBN1_30 | AATCAACCAATTGTTCCCAGGAT | GGCAATCCTTGTGGAAATGGAAC | 163 | 44 | AATCAACCAATTGTTCCCAGGATCAGTACACGTAATC | chr15 | 48726728 | 48726890 |
| FBN1 | FBN1_31 | ATTGGACCGGGCTCAAATCC | aacaacaaaaTTACAGTTTAAAATCCTCTG | 197 | 39 | ATTGGACCGGGCTCAAATCCCTCCTCGCAGGTGCATT | chr15 | 48726805 | 48727001 |
| FBN1 | FBN1_32 | ACTTATTTCAGTGCCATCTTGGT | ACATGGACAGTGCATCAATACAGA | 191 | 36 | ACTTATTTCAGTGCCATCTTGGTACCTATAYTCATGGC | chr15 | 48729050 | 48729240 |
| FBN1 | FBN1_33 | CACCTACACATTCATTCCCTGCT | TCACGTTTAAAAAATACCTTGTTATTCACT | 171 | 37 | CACCTACACATTCATTCCCTGCTAGAATATAACCAAAC | chr15 | 48729155 | 48729325 |
| FBN1 | FBN1_34 | AACTAGAGAAGAAGCAGATTGAGAA | TGTGGAGAAGCTTGTAATGAATTG | 190 | 44 | AACTAGAGAAGAAGCAGATTGAGAATACTGAGAAAT | chr15 | 48729456 | 48729645 |
| FBN1 | FBN1_35 | ACTGTCTTTAAGGCCTACAGTCTT | ACCCAAATCCAGAAATCACTCCA | 185 | 54 | ACTGTCTTTAAGGCCTACAGTCTTACTTACATCATGGC | chr15 | 48729878 | 48730062 |
| FBN1 | FBN1_36 | CATACCATCAGGTTCCGTGGG | AGTAGGAAAGCAACTGAAGGGTG | 197 | 49 | CATACCATCAGGTTCCGTGGGGCAGAGCTCGCAGGG | chr15 | 48729960 | 48730156 |
| FBN1 | FBN1_37 | AGACCACCACAAATAAACATGCAG | CCCTGGGCACATGCAGTA | 147 | 47 | AGACCACCACAAATAAACATGCAGCATTGAAAGCCC | chr15 | 48733861 | 48734007 |
| FBN1 | FBN1_38 | CTTCCACTGGAGGACAAGGAAAA | TGTGTGTCCACATTGTGTGTTTG | 196 | 43 | CTTCCACTGGAGGACAAGGAAAACCCTTCTGGACAC | chr15 | 48733929 | 48734124 |
| FBN1 | FBN1_39 | ACGTCATTACAAAAATTCTCATTCTGC | AGAACCCAGAAAATGTGCACCAG | 183 | 44 | ACGTCATTACAAAAATTCTCATTCTGCTWAGTCCAGT | chr15 | 48736656 | 48736838 |
| FBN1 | FBN1_40 | GCTTTCCTACCTTCACACTTCTC | TGTTTGATGGAAGTCATGCCAGT | 189 | 43 | GCTTTCCTACCTTCACACTTCTCATTTTGAAGACTGTA | chr15 | 48736728 | 48736916 |
| FBN1 | FBN1_41 | TGCATGATTCCTTGAGTGGTCTC | TGTGCAAGTGGAAATGGGAATCT | 182 | 46 | TGCATGATTCCTTGAGTGGTCTCTGGAAGCATTCTTT | chr15 | 48737509 | 48737690 |
| FBN1 | FBN1_42 | CATCTGGAGCCACCTCATAGC | TGCTGGGATTATGACATCTTTGGA | 172 | 41 | CATCTGGAGCCACCTCATAGCCTTCATTGCACTGGCA | chr15 | 48737588 | 48737759 |
| FBN1 | FBN1_43 | AGCTGGAACACTAGAGATGATGC | TGAAAGAGATGCCTGTGGGAATG | 189 | 42 | AGCTGGAACACTAGAGATGATGCTRATTACAAAGAA | chr15 | 48738818 | 48739006 |
| FBN1 | FBN1_44 | CACAATTTTGCACACGCACCTAT | TGTTTCTTTATGGCCTTTCTTCCT | 165 | 42 | CACAATTTTGCACACGCACCTATACAGTCATTGTTGTC | chr15 | 48738884 | 48739048 |
| FBN1 | FBN1_45 | CCATATTTAGAATCAAATGAAGCTTTCAACA | CCAATATATGCAGTCATGGGCAGT | 168 | 35 | CCATATTTAGAATCAAATGAAGCTTTCAACAGCATAT | chr15 | 48740899 | 48741066 |
| FBN1 | FBN1_46 | CAAGCACATGGTTTGGTCATCATT | TCTTCTAAGTTCTCACTTAAGATGCT | 163 | 38 | CAAGCACATGGTTTGGTCATCATTTGTTTTAAAACCA | chr15 | 48740966 | 48741128 |
| FBN1 | FBN1_47 | TCATGAAGACAAACTCTTGGGT | AGATATTGACGAGTGTCAGAACGG | 178 | 56 | TCATGAAGACAAACTCTTGGGTAGGCATGTCCAGCCT | chr15 | 48744706 | 48744883 |
| FBN1 | FBN1_48 | TACCATTGCACTGTCCTGTGGAG | TCATGTGAGAGGCTTTGTTGACT | 198 | 52 | TACCATTGCACTGTCCTGTGGAGGTGAAGCGGTAGS | chr15 | 48744756 | 48744953 |
| FBN1 | FBN1_49 | TCGCCAAGTGTGTATCAAGTAGC | GATCCCAGGGGTCTGTGAAAATG | 179 | 42 | TCGCCAAGTGTGTATCAAGTAGCTCATCAGTTAGCTC | chr15 | 48748762 | 48748940 |
| FBN1 | FBN1_50 | GCCACTTACCTTCACAAACCAAC | GATCATGTGCTGTCCTGTCACTC | 181 | 45 | GCCACTTACCTTCACAAACCAACAACTTGTCATTATAC | chr15 | 48748825 | 48749005 |
| FBN1 | FBN1_51 | TGCTAACACAAAGGCAAAAAACC | TTGTTCTTTGCTGACCCCTATCC | 179 | 44 | TGCTAACACAAAGGCAAAAAACCAGAAAGTTCTGAC | chr15 | 48752389 | 48752567 |
| FBN1 | FBN1_52 | TCGCTAAGACTGATTTCCCCAAC | CCAGACCTGTGATGGAGAATTGTTA | 195 | 43 | TCGCTAAGACTGATTTCCCCAACAATTCATGGGTAAT | chr15 | 48755200 | 48755394 |
| FBN1 | FBN1_53 | TTCACAGGGCTTGTTCCAC | TTGTGATTTCCCACATGGCATCA | 196 | 43 | TTCACAGGGCTTGTTCCACGCCCGGCCAATGTTGTAG | chr15 | 48755301 | 48755496 |
| FBN1 | FBN1_54 | TGAACTTGTGAGCTCTCTTCCTC | ATCTGTGGTCCAGGGACATGTTA | 169 | 43 | TGAACTTGTGAGCTCTCTTCCTCTTTGtagatgagaacca | chr15 | 48756024 | 48756192 |
| FBN1 | FBN1_55 | ACCCATGCAATTATTTCCCCCAT | TCAGGCCATTCCAAAATGTGAAG | 186 | 41 | acccatgcaattatttcccccattcacttgcatgtagTCTGGAGGA | chr15 | 48756094 | 48756279 |
| FBN1 | FBN1_56 | TCTGGTTTTGCAGGTCAGTTCTT | AGATATTGATGAGTGCCAGGAGC | 191 | 47 | TCTGGTTTTGCAGGTCAGTTCTTGATATCTGCAAGAC | chr15 | 48757702 | 48757892 |
| FBN1 | FBN1_57 | AGGACCATTTACCATCACACACT | ATTTCCTTGGGTTTATTTACAATGCT | 194 | 43 | AGGACCATTTACCATCACACACTCRTGTRTCTTCATTC | chr15 | 48757753 | 48757946 |
| FBN1 | FBN1_58 | GCTCCTGGCACTCATCAATATCT | TTGTTTCAATAGCCGAGTACAAAAT | 198 | 38 | GCTCCTGGCACTCATCAATATCTATCAAAATCAAAAC | chr15 | 48757870 | 48758067 |
| FBN1 | FBN1_59 | CGGTGATAGGATTTGGTCGGAAA | GGCAGAGTAACAACTAAAGATTCCTG | 186 | 34 | CGGTGATAGGATTTGGTCGGAAACCTTCCCCTCCAGC | chr15 | 48757999 | 48758184 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| FBN1 | FBN1_60 | GGAGAACTGGCTGGAGTTGAAA | CGAGGAGACAATGGAGATACAGC | 178 | 47 | GGAGAACTGGCTGGAGTTGAAATAATAATAAATAGC | chr15 | 48760084 | 48760261 |
| FBN1 | FBN1_61 | GGACACATCTCACAAGGAGTACC | TCTGCCTGATGCTTTTGTGTTTG | 188 | 46 | GGACACATCTCACAAGGAGTACCCCAGGCTTTACCCA | chr15 | 48760149 | 48760336 |
| FBN1 | FBN1_62 | TTGCAAACTTTGAGAATGGAATGT | ATCCAACCACGTGCATCAGT | 193 | 42 | TTGCAAACTTTGAGAATGGAATGTYTGGTGCTGTTTT | chr15 | 48760521 | 48760713 |
| FBN1 | FBN1_63 | TTACCAACACAGCCAACTCG | TTATGGTGATGTCTGCCTACACT | 190 | 48 | TTACCAACACAGCCAACTCGAGTTGGGTTCAGTTCAA | chr15 | 48760605 | 48760794 |
| FBN1 | FBN1_64 | TGCTTTTCTTGTCTTCTGTGACG | TCTTTGGAACTTGCCACAACCT | 198 | 57 | TGCTTTTCTTGTCTTCTGTGACGGCCCTTGTGTAGTCC | chr15 | 48762723 | 48762920 |
| FBN1 | FBN1_65 | GACACCAGGGAGCTGATTTTGAT | CCCCCAAGATATTGATGAGTGCT | 171 | 54 | GACACCAGGGAGCTGATTTTGATGCCAGTGGAGGTC | chr15 | 48762791 | 48762961 |
| FBN1 | FBN1_66 | TGGCAAGTTCCAAAGACACAGAT | AAGTGCCCAGATTGGTGTTAGAT | 178 | 36 | TGGCAAGTTCCAAAGACACAGATGTTCGGAAGGGAC | chr15 | 48762905 | 48763082 |
| FBN1 | FBN1_67 | TAACCTAATCTCATCAAGCCCAG | AGAACCTGAATCTCTGTGGCAAT | 162 | 55 | TAACCTAATCTCATCAAGCCCAGCAAGGCTCCCAGTG | chr15 | 48764694 | 48764855 |
| FBN1 | FBN1_68 | CCATCAGTTACCTTCACAGGCTT | CCGAGGAAGAGTAACGTGTGTTT | 174 | 53 | CCATCAGTTACCTTCACAGGCTTTCCCGTCAGCACTG | chr15 | 48764737 | 48764910 |
| FBN1 | FBN1_69 | TTGCTAGCCTGAGAAATGTGGAA | TCCAATGGAACCCATATGTGCAG | 184 | 48 | TTGCTAGCCTGAGAAATGTGGAATGCCTGGCTTCTCT | chr15 | 48766377 | 48766560 |
| FBN1 | FBN1_70 | TTTCCAGCGTGAACATACCTGT | GTTTTAAATACCACCCTTTCTGTTAATAATG | 192 | 42 | TTTCCAGCGTGAACATACCTGTACAAGTGAAGCCATC | chr15 | 48766434 | 48766625 |
| FBN1 | FBN1_71 | TCATATGTGTAATCTATGCAGTCCTT | TGTGAAATTGGAGCACACAACTG | 169 | 44 | TCATATGTGTAATCTATGCAGTCCTTGATAAGCAACC | chr15 | 48766668 | 48766836 |
| FBN1 | FBN1_72 | GCACTTAATGCCATCTCCAATCC | AGACATTTGTGCTGAGCCTTTTT | 166 | 43 | GCACTTAATGCCATCTCCAATCCACCCGGGACTGCAG | chr15 | 48766729 | 48766894 |
| FBN1 | FBN1_73 | GGAAGCTAAATTAATGAAAAATGTTATGCAA | CTGCCACTGTGATATGGGCTAC | 198 | 29 | GGAAGCTAAATTAATGAAAAATGTTATGCAAAATGT | chr15 | 48773707 | 48773904 |
| FBN1 | FBN1_74 | ACAGCCAGTTTTTCCTTTTTTGC | TCCAAATATCTGCCTAAGTGGGAC | 100 | 45 | ACAGCCAGTTTTTCCTTTTTTGCCGGAGTAGCCCATAT | chr15 | 48773856 | 48773955 |
| FBN1 | FBN1_75 | TTTTTGCCGGAGTAGCCCATATC | ATGTCTCGAGGGGAAAGTACTCA | 175 | 38 | TTTTTGCCGGAGTAGCCCATATCACAGTGGCAGATAA | chr15 | 48773872 | 48774046 |
| FBN1 | FBN1_76 | AATCTTTCTATCACTGACCCAAACT | TCCCAATATCTGTGATGGTGGTC | 198 | 38 | AATCTTTCTATCACTGACCCAAACTAACTTTATGTAAT | chr15 | 48775921 | 48776118 |
| FBN1 | FBN1_77 | ATGTCTTCAGATGCCATGAATCC | ACTGCGGTCAGTTAATGTTTTCT | 192 | 42 | ATGTCTTCAGATGCCATGAATCCATCATAACACAAGC | chr15 | 48776029 | 48776220 |
| FBN1 | FBN1_78 | TGACAAACAAGGGTTTGGACTCA | CTTCTGCACAAACTCTGAAGGC | 193 | 48 | tgacaaacaagggtttggactcaagcctgcttgactccaaagcctgg | chr15 | 48777461 | 48777653 |
| FBN1 | FBN1_79 | ACTGAGAGATTCAACATGAGGCTA | aaccatatcaGAAGGTGATATTATTTTCATT | 198 | 41 | ACTGAGAGATTCAACATGAGGCTAGAACMTACWCA | chr15 | 48777535 | 48777732 |
| FBN1 | FBN1_80 | ACTCAGAGTACATAGAGTGTTTTAGG | GTGAACCTCATAGGGAAGTATCAGT | 198 | 28 | ACTCAGAGTACATAGAGTGTTTTAGGKAGAGatgaaa | chr15 | 48779150 | 48779347 |
| FBN1 | FBN1_81 | GCCTATCGGGAGTTGAATGGTAG | ACATCATTGCCAAAGTTGGAAGC | 175 | 48 | GCCTATCGGGAGTTGAATGGTAGCCAGGGTTGCAGC | chr15 | 48779284 | 48779458 |
| FBN1 | FBN1_82 | ACACCCAAACATAAGCTTCCAAC | AGAGATCCTCTCCTATGCCGAG | 196 | 48 | ACACCCAAACATAAGCTTCCAACTTTGGCAATGATGT | chr15 | 48779422 | 48779617 |
| FBN1 | FBN1_83 | ACCACAAGTAAATGGTGTGAAAGT | CCCCCACCTTTAACATGGTCATT | 197 | 49 | ACCACAAGTAAATGGTGTGAAAGTCTTTCTCCTYACC | chr15 | 48779473 | 48779669 |
| FBN1 | FBN1_84 | TCAAAGCTTCATGGAATCCTTCTCT | TGTTTTTGTGCAGACATTGACGA | 198 | 44 | TCAAAGCTTCATGGAATCCTTCTCTTTCTGTGTTGATC | chr15 | 48780254 | 48780451 |
| FBN1 | FBN1_85 | ATCCCAAACTTACCCATGCAGTT | GCAAGAATTAAGGCTGTCCTGAGA | 198 | 47 | ATCCCAAACTTACCCATGCAGTTCTTCATCATCAKGAA | chr15 | 48780297 | 48780494 |
| FBN1 | FBN1_86 | GGACAGCCTTAATTCTTGCGACA | CACGGCAAGTGCAGAAACAC | 177 | 45 | GGACAGCCTTAATTCTTGCGACAATATGTTAAAGATA | chr15 | 48780476 | 48780652 |
| FBN1 | FBN1_87 | GGCTCATTAACTGACCTGTGC | ACTTATTTTGCCCCACATTTTCTT | 175 | 45 | GGCTCATTAACTGACCTGTGCAGTTCNNNNNTTCAG | chr15 | 48780550 | 48780724 |
| FBN1 | FBN1_88 | AAGTAGAGTGCTGAGATCATGAAA | GGTACTGAGGAATGCGAGGA | 200 | 43 | AAGTAGAGTGCTGAGATCATGAAAATGCATCCTATTT | chr15 | 48781966 | 48782165 |
| FBN1 | FBN1_89 | GGTCCTCTCGGACACAGCTC | CTGACAGATATCCGCCTGGAAAC | 188 | 61 | GGTCCTCTCGGACACAGCTCCTCGTACTCAGGAGTAT | chr15 | 48782095 | 48782282 |
| FBN1 | FBN1_90 | CTCCTCGCATTCCTCAGTACC | GTTGGCAGTTTGGGGCAGT | 196 | 60 | CTCCTCGCATTCCTCAGTACCCCAGGCTGCCCCGACG | chr15 | 48782145 | 48782340 |
| FBN1 | FBN1_91 | CTGTACCTGAAGCTAAGTGCTCA | GGAGTGTGTAAAAATGGCCTGTG | 198 | 37 | CTGTACCTGAAGCTAAGTGCTCARCTATATCTTGTTAA | chr15 | 48784560 | 48784757 |
| FBN1 | FBN1_92 | GACAGATCCTTCCTGTGGCATC | TGACTCTATGAGTAGAATAAGGTAGAATGA | 197 | 36 | GACAGATCCTTCCTGTGGCATCCAAAGTCATTCCACT | chr15 | 48784661 | 48784857 |
| FBN1 | FBN1_93 | CTCTGCTGCATATTTCTCCCTGT | TGTTTTCTGTTTTGTTTTTCGCTTT | 198 | 34 | CTCTGCTGCATATTTCTCCCTGTGAAGTTATATGACAC | chr15 | 48786288 | 48786485 |
| FBN1 | FBN1_94 | ACTAGGCTTCCCCTTTTTATGCAA | GTGAGATCAACATCAATGGAGCC | 162 | 52 | ACTAGGCTTCCCCTTTTTATGCAAAGACCATTGGAGT | chr15 | 48787251 | 48787412 |
| FBN1 | FBN1_95 | GCTTCCCCACGCAGCA | TGTCTATAATTCCAAGGTGTATGTTTGA | 187 | 44 | GCTTCCCCACGCAGCACCGAGGGAGGAGCAGCACTG | chr15 | 48787342 | 48787528 |
| FBN1 | FBN1_96 | TTGCAGGAAAAGCTGACATTAAG | TTGATGAATGCGAATCAAGTCCT | 190 | 35 | TTGCAGGAAAAGCTGACATTAAGTATAACAACATTGA | chr15 | 48787593 | 48787782 |
| FBN1 | FBN1_97 | GGCTGTTCTTGCAGACTCCATT | ATTTAGCCCAGCTTTACTGTGTG | 176 | 40 | GGCTGTTCTTGCAGACTCCATTAATGCAAGGACTTGA | chr15 | 48787732 | 48787907 |
| FBN1 | FBN1_98 | TGGCATTCCAAAAGATAGCAAAG | TGAATGTGTACTGAACAGTCTCC | 173 | 37 | TGGCATTCCAAAAGATAGCAAAGTACACAGTATAAG | chr15 | 48788243 | 48788415 |

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| FBN1 | FBN1_99 | ACCTTCACATGTTTTTAGATCAGGTTT | AGGCAAAGTTTGGGCCCTTTTTA | 177 | 37 | ACCTTCACATGTTTTTAGATCAGGTTTGTAGATAAAT( | chr15 | 48788295 | 48788471 |
| FBN1 | FBN1_100 | ATTTGCCCAGTCCTCTAAGCTAC | TGCCCAAATGGAATCTGTGAAAAC | 198 | 41 | ATTTGCCCAGTCCTCTAAGCTACTCAAAGGCAGTTTTT( | chr15 | 48789359 | 48789556 |
| FBN1 | FBN1_101 | CTTCTCACCAACGCAGTTTTTCC | TCTTAATTGATTTTGACCTTTTTTGTGGT | 167 | 37 | CTTCTCACCAACGCAGTTTTTCCCAGTTGAATCCACTT | chr15 | 48789455 | 48789621 |
| FBN1 | FBN1_102 | CAACTGGAAACCCACAAGAAAGC | CAAGGGCAGGATCTACCTGTTC | 195 | 46 | CAACTGGAAACCCACAAGAAAGCCTGATGCTGCCTCT | chr15 | 48791105 | 48791299 |
| FBN1 | FBN1_103 | AAAGACCTCAATGGTGGCAGAAG | GCTATGGTGGATACAAGAGAGGC | 192 | 49 | AAAGACCTCAATGGTGGCAGAAGGCTGGCAGTACGA | chr15 | 48795924 | 48796115 |
| FBN1 | FBN1_104 | AAGGTTCCCCAAATGCATACTCA | GTGACAGTGTGATGACAGATGCT | 162 | 46 | AAGGTTCCCCAAATGCATACTCAGTGCTGGCRCAACA | chr15 | 48796011 | 48796172 |
| FBN1 | FBN1_105 | CCATTGGGCTTTATTGAGTGACAG | TGAAACCCCTGGGATCTGCAT | 177 | 50 | CCATTGGGCTTTATTGAGTGACAGAGGCTGAACCTCT | chr15 | 48797155 | 48797331 |
| FBN1 | FBN1_106 | TGTTTTCTTACCAACACACACACG | ACTTCATTTTTAATAAGTGCCTTTCTCT | 169 | 49 | TGTTTTCTTACCAACACACACACGGCCATCCAGACCCA | chr15 | 48797211 | 48797379 |
| FBN1 | FBN1_107 | ACAACATAAGGAGGAGAAAAGGC | GGATGAATGCAGCATAAGGAACA | 179 | 40 | ACAACATAAGGAGGAGAAAAGGCAYGTGAAGAACA | chr15 | 48800719 | 48800897 |
| FBN1 | FBN1_108 | CGAACCTTTGCAATAACGTCCAT | TCATCCAGATTGGTTTCCTTCGT | 198 | 38 | CGAACCTTTGCAATAACGTCCATCTGATGCCAGCTGG | chr15 | 48800774 | 48800971 |
| FBN1 | FBN1_109 | CCCCTGATATTGAAACTGCAATGG | GTGTTTACAGAATGGCCGGATCT | 174 | 43 | CCCCTGATATTGAAACTGCAATGGAAGGAGAGGACT | chr15 | 48802183 | 48802356 |
| FBN1 | FBN1_110 | TTCACAGTTCTTCCCATCTCGTG | ACTCCCCTAAATAAAGCTATTTCTTCT | 171 | 40 | TTCACAGTTCTTCCCATCTCGTGTAACATGAAAGCCC( | chr15 | 48802242 | 48802412 |
| FBN1 | FBN1_111 | GTCTCTTCCGGCATGGGTTATTT | TGGTGAGTGTATTAACAACCAGGG | 189 | 51 | GTCTCTTCCGGCATGGGTTATTTAAACTCCAYGGAAC | chr15 | 48805643 | 48805831 |
| FBN1 | FBN1_112 | CATTCTGTCCGCGTGAGTGT | CCCAGAAAGTCTTAGAATTATGAGGTA | 183 | 43 | CATTCTGTCCGCGTGAGTGTGCTCTGATATCCAGCTC | chr15 | 48805751 | 48805933 |
| FBN1 | FBN1_113 | aGAGTCAAGGAACAGAATTACAACA | CGTTACTGATTACTGCCAGTTGGT | 184 | 51 | aGAGTCAAGGAACAGAATTACAACAGACCCTTGGTG | chr15 | 48807525 | 48807708 |
| FBN1 | FBN1_114 | GCTGGAACCCTTTGTTGCAC | TGTCAGATTAAGTACTGATGAAAGATACCA | 186 | 43 | GCTGGAACCCTTTGTTGCACTCACACCGGYAACTCCC | chr15 | 48807608 | 48807793 |
| FBN1 | FBN1_115 | TGAACAATGCAAGAAAAATAACTAGATGA | AGACCAGAATATCCTCCCCCAC | 180 | 49 | TGAACAATGCAAGAAAAATAACTAGATGATTTTTGAA | chr15 | 48808336 | 48808515 |
| FBN1 | FBN1_116 | GGTCGAGGGACCGGAATTTG | AGCTCAGCTGTTGTGTTTTGTTT | 181 | 51 | GGTCGAGGGACCGGAATTTGAGGTCCAGGAGGAAA | chr15 | 48808418 | 48808598 |
| FBN1 | FBN1_117 | ACCCAAGTTTCCATTACATCTGC | TGCCACAGTCCATAACCAAAATG | 197 | 54 | ACCCAAGTTTCCATTACATCTGCATCATGCACATTGCC | chr15 | 48812761 | 48812957 |
| FBN1 | FBN1_118 | TCTGATGGGACACATCTCAGGG | TCAGCGATGTGTGTGTGTATG | 192 | 53 | TCTGATGGGACACATCTCAGGGGCGACAGTGACCCC | chr15 | 48812863 | 48813054 |
| FBN1 | FBN1_119 | ACCTCAGTTGATAAATTATATGTGCTCCT | AATGTACAAACACAGTCAGCAGT | 188 | 38 | ACCTCAGTTGATAAATTATATGTGCTCCTTAACAAGC | chr15 | 48818220 | 48818407 |
| FBN1 | FBN1_120 | GGTACCATCTGGAGAGGTGTAAA | ACATCTGAGTCCTTCTACTGACGA | 193 | 40 | GGTACCATCTGGAGAGGTGTAAAAACCAGGGGGAC/ | chr15 | 48818337 | 48818529 |
| FBN1 | FBN1_121 | TTTTGCCTGCCCCCACTAC | TCTGACAGATGTGGATGAATGCC | 185 | 47 | TTTTGCCTGCCCCCACTACACCCCCCAACTGCAAAGC/ | chr15 | 48826226 | 48826410 |
| FBN1 | FBN1_122 | CAATTTCCTCCCTGACAGAGCC | TGTGATGGACAAATAACTCACCGA | 176 | 35 | CAATTTCCTCCCTGACAGAGCCCGGGGATGGCCTGG( | chr15 | 48826354 | 48826529 |
| FBN1 | FBN1_123 | AGCTGACACTACTTTTCCATTCTCT | CCCTGTGAGATGTGTCCTG | 178 | 49 | AGCTGACACTACTTTTCCATTCTCTTCAACTTCATTGG | chr15 | 48829709 | 48829886 |
| FBN1 | FBN1_124 | CAGGGGTGAGGCTGGG | TGCTTTTCTGGATTTTCATCAGATTTT | 197 | 50 | CAGGGGTGAGGCTGGGCAGGACACATCTCACAGGG | chr15 | 48829852 | 48830048 |
| FBN1 | FBN1_125 | AGTAACAGCTTTAGGTACCAGCA | GCGTCTCAGCTCTCTCCTTATTT | 180 | 43 | AGTAACAGCTTTAGGTACCAGCATGTCTTTAYGTAAA | chr15 | 48888424 | 48888603 |
| FBN1 | FBN1_126 | TAAACATGCTGTGTCCCAGGTAA | AATATTCGCTGTATGAATGGAGGT | 198 | 39 | TAAACATGCTGTGTCCCAGGTAATCGARGAAAATCCA | chr15 | 48892223 | 48892420 |
| FBN1 | FBN1_127 | CTTACGTTGTCCACAGTGAGTCC | CTCCTGTGAGCTGTTGCAATCTA | 168 | 41 | CTTACGTTGTCCACAGTGAGTCCCTATGTATCCTTTCT | chr15 | 48892331 | 48892498 |
| FBN1 | FBN1_128 | ATTGCAGGAAAGAGGAAAGCCAA | TTCCTGTGGGGATGGATTTTGTT | 180 | 39 | ATTGCAGGAAAGAGGAAAGCCAAAATCAAATTTAGC | chr15 | 48902831 | 48903010 |
| FBN1 | FBN1_129 | CCACAGGAAGGAGCTATCTGAC | ctcattTGAGGATTGGTCCCCTA | 164 | 47 | CCACAGGAAGGAGCTATCTGACCAGATGGRCAAGTG | chr15 | 48902936 | 48903099 |
| FBN1 | FBN1_130 | AGGACATGCAGAATGACAAGTTT | TGGCCATCTCTTCCTCTTCTTCT | 180 | 37 | AGGACATGCAGAATGACAAGTTTTCTATTTACTTAYG | chr15 | 48905171 | 48905350 |
| FBN1 | FBN1_131 | CCGTTGTTCTGGATCTTGAAACT | ATTTACCGTGCTTTTAGCGTCCT | 191 | 55 | CCGTTGTTCTGGATCTTGAAACTTGGGAGACCCACAC | chr15 | 48936741 | 48936931 |
| FBN1 | FBN1_132 | CCTCCACCGCCTCTTCTCTT | TGGCGGCTCGGCATCA | 161 | 61 | CCTCCACCGCCTCTTCTCTTGGCCCGACTGGCTCTGGT | chr15 | 48936821 | 48936981 |
| FBN1 | FBN1_133 | GGACGCTAAAAGCACGGTAAATC | GACGGGCGGCGGGATA | 175 | 75 | GGACGCTAAAAGCACGGTAAATCCCAGGGCGATCTC | chr15 | 48936910 | 48937084 |
| MYH11 | MYH11_1 | CGCATTGGGCAGAAAAGAAATGG | ATACTTAACCGGGCTCCTTCTTG | 168 | 52 | CGCATTGGGCAGAAAAGAAATGGATACTGAGACAAC( | chr16 | 15802595 | 15802762 |
| MYH11 | MYH11_2 | CATTTGCAGGCCGAAAGGAG | GAGTCCCAGCGCATCAACG | 198 | 66 | CATTTGCAGGCCGAAAGGAGCCCGAGCCCCCAGTGC | chr16 | 15808681 | 15808878 |
| MYH11 | MYH11_3 | CCCATGGCCTCGTTGCTC | AGCCGGCCTCCCCTAAC | 181 | 64 | CCCATGGCCTCGTTGCTCTCCGTGGCCTCATCCAGCT( | chr16 | 15808799 | 15808979 |
| MYH11 | MYH11_4 | TGGGTGGCAGGGGCTA | CAGGTGACACACCAGCTACAAG | 195 | 56 | TGGGTGGCAGGGGCTACCTGCTCCTTGTACTGCTCG( | chr16 | 15809004 | 15809198 |

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| MYH11 | MYH11_5 | CACTATGACTCCTGCTGTCCATC | GAGCGGCAGAACAAGGAGC | 198 | 61 | CACTATGACTCCTGCTGTCCATCACCCCCCTGCAAACT | chr16 | 15810933 | 15811130 |
| MYH11 | MYH11_6 | TTGACGGCCCCCTCCATC | TCTTGGGCTTCCCTGAGTCC | 179 | 64 | TTGACGGCCCCCTCCATCTCGTGGAGCTTGCTCCGGA | chr16 | 15811075 | 15811253 |
| MYH11 | MYH11_7 | TGCTGCAGGAGAGACAGTAGG | AACGCACTCCAGGACGAGAAG | 176 | 66 | TGCTGCAGGAGAGACAGTAGGCAGCGTGACTGTGG | chr16 | 15812119 | 15812294 |
| MYH11 | MYH11_8 | GCCCTCACCTGCTGTGT | GTAGAGGCCCCCACCAT | 166 | 69 | GCCCTCACCTGCTGTGTGGCTTTGCGGACCCGGTCGC | chr16 | 15812164 | 15812329 |
| MYH11 | MYH11_9 | GTCCCCCCATCCTCTGCTT | AGACAACAGCCTTCCTCCCT | 168 | 61 | GTCCCCCCATCCTCTGCTTCAGAGCCCTCTTCCTCCAT | chr16 | 15813027 | 15813194 |
| MYH11 | MYH11_10 | AGGAGGACGAAATGAAATCTGGG | CCGTGCCTCCAGAGATGAGAT | 192 | 54 | AGGAGGACGAAATGAAATCTGGGAATGCACAGACTC | chr16 | 15813341 | 15813532 |
| MYH11 | MYH11_11 | CGAGGCTTTACCTCTTGTAGCTG | GGGAGTAAGGACATCTGAGCTTG | 185 | 51 | CGAGGCTTTACCTCTTGTAGCTGCATGAGGTCTGCTT | chr16 | 15813431 | 15813615 |
| MYH11 | MYH11_12 | GGCCTGAGGGGAACTGTG | GAAGACGAGCGAAAGCAACG | 197 | 60 | GGCCTGAGGGGAACTGTGCCCTCCCTCCACCCATGCC | chr16 | 15813949 | 15814145 |
| MYH11 | MYH11_13 | CAGTTTGCGTAGCTGCTTGATG | GGCAGCACACATCTCTATTCCTC | 188 | 57 | CAGTTTGCGTAGCTGCTTGATGGCTTCCTCCCTCCCCT | chr16 | 15814011 | 15814198 |
| MYH11 | MYH11_14 | GATAGGAATGAAAAAGGCCACCC | TGGAGGACGAGCTGCAAG | 198 | 61 | GATAGGAATGAAAAAGGCCACCCGACCTCCCTCTGC | chr16 | 15814638 | 15814835 |
| MYH11 | MYH11_15 | TTTCGAACTGGCCCTTGAGC | TGAAGTTGAGCCTCATAGAATGG | 198 | 61 | TTTCGAACTGGCCCTTGAGCGCCTGCATGTTGACTTC | chr16 | 15814755 | 15814952 |
| MYH11 | MYH11_16 | GGTGAATAGCACAGAGGGTGG | AAACCAAGGCCCTGTCCC | 198 | 55 | GGTGAATAGCACAGAGGGTGGGCAGGCGAAACATG | chr16 | 15815215 | 15815412 |
| MYH11 | MYH11_17 | AGGTCTTCCATTTCGGCTTTGAG | GTTGTAGTTGTTAGCCGAGGAGA | 189 | 52 | AGGTCTTCCATTTCGGCTTTGAGCAYTTTGTTGGTCCC | chr16 | 15815310 | 15815498 |
| MYH11 | MYH11_18 | CTTTGGCTTCCAAGGCCTCTTC | TTACAATTCAGTGACGCTGACCC | 196 | 53 | CTTTGGCTTCCAAGGCCTCTTCAAGGGCCCGAGCCAG | chr16 | 15815359 | 15815554 |
| MYH11 | MYH11_19 | CTGCAGAGCTGATTCCCCAAC | TGGAAAAGACCAAGAACAGGCTT | 177 | 55 | CTGCAGAGCTGATTCCCCAACCCAGCGTCCATGGCCA | chr16 | 15817954 | 15818130 |
| MYH11 | MYH11_20 | GCCCTCTACCTGATCAAATTTCC | GGAAGAAGAGGTTCCAGAAGGAG | 197 | 52 | GCCCTCTACCTGATCAAATTTCCTCTGCTTCTTTTCCA | chr16 | 15818009 | 15818205 |
| MYH11 | MYH11_21 | AAGCCTGTTCTTGGTCTTTTCCA | CTACCCTGGACGCTGTCCTT | 183 | 54 | AAGCCTGTTCTTGGTCTTTTCCAGTTTATCATANGCG | chr16 | 15818108 | 15818290 |
| MYH11 | MYH11_22 | GCGCAGAGAAGTTGAGAGGAC | TCAAGAAGAAACCCGGCAGAA | 198 | 59 | GCGCAGAGAAGTTGAGAGGACCCATGAAGGAAGCA | chr16 | 15818451 | 15818648 |
| MYH11 | MYH11_23 | ACCTGGATGTTGAGAGTGGAGAT | GGGACCTCTTTGCATCCCTTT | 181 | 57 | ACCTGGATGTTGAGAGTGGAGATGTGGCGCTCCAGC | chr16 | 15818502 | 15818682 |
| MYH11 | MYH11_24 | CAGGTCCCCTGGATGATGTG | ATCCCCTTCTAGAGGCTTTGACT | 184 | 56 | CAGGTCCCCTGGATGATGTGGCAGGACACTCACCTG | chr16 | 15818712 | 15818895 |
| MYH11 | MYH11_25 | gaggctcctCCCCACAGAA | CCAAGCAGGAGGTGGAACA | 190 | 62 | gaggctcctCCCCACAGAACTGGGCACCACCCAGCACTC | chr16 | 15820637 | 15820826 |
| MYH11 | MYH11_26 | CCATCGCTGCACTTGGACTG | CCCTCCCCTCTGCTTCCTTC | 186 | 61 | CCATCGCTGCACTTGGACTGCAGCTCCTGCACCTGCG | chr16 | 15820751 | 15820936 |
| MYH11 | MYH11_27 | ACCTGTAGTAATTTGAGGCTGCT | GAAGAAGGCCCTGGATGAAGAGA | 188 | 52 | ACCTGTAGTAATTTGAGGCTGCTGATGTCACTCTTAY | chr16 | 15826348 | 15826535 |
| MYH11 | MYH11_28 | AGCATCACCAAAAAGCATTACCC | AACTGCCATTCACTGTGTTCCTC | 197 | 57 | AGCATCACCAAAAAGCATTACCCTCTTGAACTGCTCA | chr16 | 15826400 | 15826596 |
| MYH11 | MYH11_29 | ACGATTTGCTTTGGGTTTGTCC | GCCAGGAACAAGGCTGAAAAG | 198 | 58 | ACGATTTGCTTTGGGTTTGTCCCCTCTTCTGCCCCCAT | chr16 | 15829135 | 15829332 |
| MYH11 | MYH11_30 | GTGTGTCTTCCAGCTCTGTCTTT | CCTGGAAGGCTTGACGATGAAAT | 190 | 57 | GTGTGTCTTCCAGCTCTGTCTTTAGGGCCTCCAGCTCC | chr16 | 15829254 | 15829443 |
| MYH11 | MYH11_31 | CTTCTGCTTTTCAGCCTTGTTCC | GCCACATTGTAAGAGAGGAAACC | 195 | 55 | CTTCTGCTTTTCAGCCTTGTTCCTGGCGGCCCGCTCTG | chr16 | 15829306 | 15829500 |
| MYH11 | MYH11_32 | GCCCAGGGGATACATGGACA | GAAGCTGAAACGGAAGCTGGAG | 183 | 63 | GCCCAGGGGATACATGGACACACAGCAAATGCCCCT | chr16 | 15831255 | 15831437 |
| MYH11 | MYH11_33 | GCAGCTCCTCCTCCTTCTTG | CTTCCTGAAGAGCACCTTGGTTT | 185 | 56 | GCAGCTCCTCCTCCTTCTTGGCCAGCTGCATCTTGAG | chr16 | 15831322 | 15831506 |
| MYH11 | MYH11_34 | aataaaaaTAAATCTCTTGGTAGCTGGTT | CCCCAAAAAGGAACGAAAACTCC | 166 | 38 | aataaaaaTAAATCTCTTGGTAGCTGGTTTACCTTCCAG | chr16 | 15832390 | 15832555 |
| MYH11 | MYH11_35 | AGCTTGGTAAGATTCTTGGCCTT | GGGTTTTTCTTTCAACTGTTTACATGG | 189 | 37 | AGCTTGGTAAGATTCTTGGCCTTTTCTTCCTCTTCTGC | chr16 | 15832460 | 15832648 |
| MYH11 | MYH11_36 | AGACACTGGCCACCACA | TCATGGATGATCAGAACAATAAACTATCAA | 200 | 49 | agacactggccaccacacctggctaatctttgtatttttagtagagatg | chr16 | 15833740 | 15833939 |
| MYH11 | MYH11_37 | cccggccCCTACTCACTT | CCTTGAAGAACAGCTGGAGGAG | 152 | 51 | cccggccCCTACTCACTTTTGATAGTTTATTGTTCTGATC | chr16 | 15833892 | 15834043 |
| MYH11 | MYH11_38 | CCAGGATCTCATCCTCCAGTTTC | GGCCTAGCCCCTGTATTCATTAG | 197 | 50 | CCAGGATCTCATCCTCCAGTTTCTTGATCTTGGCCTCA | chr16 | 15833940 | 15834136 |
| MYH11 | MYH11_39 | CCTGTGGTGAGGGTCAAGTG | CTGGCGGCCAAGAAGCAG | 182 | 60 | cctgtggtgagggtcaagtgaTTTGCTACCCACCACGGGCTC | chr16 | 15835261 | 15835442 |
| MYH11 | MYH11_40 | CTGCTGGCCCCTGTCTTC | CCTCCTCCCCACCACCT | 193 | 63 | CTGCTGGCCCCTGTCTTCCTCCTCCTCCAGGCGGGCCT | chr16 | 15835359 | 15835551 |
| MYH11 | MYH11_41 | CGGGGCCAAGTCCTGTTC | GTGTGCAGGTGAAGCCACT | 192 | 58 | CGGGGCCAAGTCCTGTTCCCCAGCAACCCCAGCCATC | chr16 | 15835565 | 15835756 |
| MYH11 | MYH11_42 | TTCTGTTCCAGCTCCTTAAGCTC | TCCCTTTGCCACAAAAACAAATGA | 168 | 54 | TTCTGTTCCAGCTCCTTAAGCTCATTCTCTGCCTTCTG | chr16 | 15835627 | 15835794 |
| MYH11 | MYH11_43 | TGTGAAGGCTCCAGAGTGAA | CCTTCTCTTCCCCCCTCC | 200 | 60 | TGTGAAGGCTCCAGAGTGAAGAASCAGGGCTGGGG | chr16 | 15838917 | 15839116 |

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| MYH11 | MYH11_44 | tcagggaaTCAGAACAGAAAGGC | AGCAAAATCTTCTTCCGAACTGG | 191 | 50 | tcagggaaTCAGAACAGAAAGGCCCCTGTTTGTGATTC | chr16 | 15841352 | 15841542 |
| MYH11 | MYH11_45 | TCTTTACTTTCTGGCCAAGTAGC | GGAGCTCTTCCTTTCCTTCCTTT | 196 | 51 | TCTTTACTTTCTGGCCAAGTAGCCACGACACATCGCC | chr16 | 15841420 | 15841615 |
| MYH11 | MYH11_46 | GCCAGTGATGACATGGGTAAGAA | GGGTGACTTCTGCTCTGTGTT | 190 | 58 | GCCAGTGATGACATGGGTAAGAACGGTCCCACCAAG | chr16 | 15841637 | 15841826 |
| MYH11 | MYH11_47 | CTCGTAGCTTGAAACACAGAGCA | TGCAATGGGGTGCTGGAAG | 190 | 60 | CTCGTAGCTTGAAACACAGAGCAGAAGTCACCCCGG | chr16 | 15841794 | 15841983 |
| MYH11 | MYH11_48 | CAGACCTTGGGACTTACCGTTG | ATCCACTGCCCTCTTTGACCTTT | 166 | 60 | CAGACCTTGGGACTTACCGTTGGCGGAACTCCTGGA | chr16 | 15841887 | 15842052 |
| MYH11 | MYH11_49 | CTGTGACCGCTTGGGACAG | CCAAGACCAAGAAGGGCATGTTC | 193 | 63 | CTGTGACCGCTTGGGACAGCCCTGGYTTCTGGRAGC | chr16 | 15843933 | 15844125 |
| MYH11 | MYH11_50 | GCGTAGCGTGGTCATCAG | CCTATTTAGGGGTGGGTGGG | 198 | 63 | GCGTAGCGTGGTCATCAGCTTGCCCAGCTGCTCCTTG | chr16 | 15844046 | 15844243 |
| MYH11 | MYH11_51 | CATGTAAAGGCCTCCCCTCCT | AGAATATGGACCCGCTGAATGAC | 189 | 56 | CATGTAAAGGCCTCCCCTCCTGGGGCAGGTGTGAGA | chr16 | 15847146 | 15847334 |
| MYH11 | MYH11_52 | CTTACCGTCCTTCCACAGGTC | TCCTGGCCTTGGTTTCTAAGTTT | 185 | 54 | CTTACCGTCCTTCCACAGGTCGGCCACAAACTTGTCG | chr16 | 15847246 | 15847430 |
| MYH11 | MYH11_53 | GCGCTGAGCAGCCACT | GAATGCTGGTTCCCCAAAGC | 198 | 60 | GCGCTGAGCAGCCACTGGGGGTCCCCTGAGACAGAC | chr16 | 15850138 | 15850335 |
| MYH11 | MYH11_54 | AACTCAGTCTTGTCCTTGAGCTG | GATTCAAGCCCTACTTGTCTCCC | 176 | 57 | AACTCAGTCTTGTCCTTGAGCTGCTTGGGCTTCTGGA | chr16 | 15850223 | 15850398 |
| MYH11 | MYH11_55 | CTCCACAGAGGCCACACAC | TTCAACCACACCATGTTCATCCT | 181 | 61 | CTCCACAGAGGCCACACACGTGTACAAGGTGTGACR | chr16 | 15851620 | 15851800 |
| MYH11 | MYH11_56 | GTCCAGCCCAAAGTCGATGAAG | TGACTTCATACCAAGATGCTCAC | 190 | 56 | GTCCAGCCCAAAGTCGATGAAGTTCCACTCGATGCCC | chr16 | 15851717 | 15851906 |
| MYH11 | MYH11_57 | AAAAGCCCATCTCAGACAACCAA | CAACATATGAGCGCCTTTTCCG | 178 | 53 | AAAAGCCCATCTCAGACAACCAAGACCATGGCTCTTA | chr16 | 15853377 | 15853554 |
| MYH11 | MYH11_58 | TATATCCAGGATCCCCAGGAAGG | AGCCTGGCTTATGTGAAAATGGA | 197 | 55 | TATATCCAGGATCCCCAGGAAGGMAGCCCCTTGCCG | chr16 | 15853454 | 15853650 |
| MYH11 | MYH11_59 | TGAGTGAACAGGTGGATAGATGG | GCCACCTCATGGGAATTAATGTG | 182 | 46 | tgagtgaacaggtggatagatggatgaatggatggatgggtgggtg | chr16 | 15854319 | 15854500 |
| MYH11 | MYH11_60 | TGTCTGAGCTTTCTGTACCACAT | TCCCATGCGATGTGTCTTCTTG | 183 | 45 | TGTCTGAGCTTTCTGTACCACATCTCGCCCAACCTTGA | chr16 | 15854406 | 15854588 |
| MYH11 | MYH11_61 | CCAGTGGTTAAATGTCACCTCCC | CTCTGCCCTTCTCTCCCCAC | 195 | 51 | CCAGTGGTTAAATGTCACCTCCCCCACCCCCCCAACCC | chr16 | 15857579 | 15857773 |
| MYH11 | MYH11_62 | TCTGTCCTGACCAGAGAAGAGTT | CTTCCTCTCCAATGGCTTTGTGC | 194 | 53 | TCTGTCCTGACCAGAGAAGAGTTCTTAACAGGTTCCA | chr16 | 15865342 | 15865535 |
| MYH11 | MYH11_63 | AAGGTGTGAGGCTTACATAGCTG | TATTGACCCTGACCTGTCTTCCT | 193 | 52 | AAGGTGTGAGGCTTACATAGCTGCTCCTCCTCGCTGA | chr16 | 15865410 | 15865602 |
| MYH11 | MYH11_64 | TCTGATGAAAGGGAAGGCTCAAG | TATCCCCAGAATCCCTAACTCCC | 188 | 46 | TCTGATGAAAGGGAAGGCTCAAGCCATCCAATCACA | chr16 | 15869879 | 15870066 |
| MYH11 | MYH11_65 | AAGATAGAGGTGGCTCTTGGACT | CAGCAAAGCCTGAACTGTGTTTT | 193 | 55 | AAGATAGAGGTGGCTCTTGGACTCTCCCAGCCTCTGC | chr16 | 15872542 | 15872734 |
| MYH11 | MYH11_66 | CAGGCAGGAGATGACACCAAAG | CCTAGGTTGCTTTCTCCAATAACT | 193 | 45 | CAGGCAGGAGATGACACCAAAGCTTTTCTGGAAAAn | chr16 | 15876185 | 15876377 |
| MYH11 | MYH11_67 | AAACTCTAGGGCCTACCCCATTT | TGTGATGGAAATAACGCTGACAT | 198 | 47 | AAACTCTAGGGCCTACCCCATTTCTACCASCAGCTAYR | chr16 | 15878430 | 15878627 |
| MYH11 | MYH11_68 | CTGGAGACCGGTTGGCTAAA | CCATGGAACGTGTGCATAGATGA | 195 | 54 | CTGGAGACCGGTTGGCTAAATCATGGCCTCTGATTGC | chr16 | 15880436 | 15880630 |
| MYH11 | MYH11_69 | CTCTGCACTCATGGATCTTTTCT | CCAAGTCCAGACCCTTAGCTC | 198 | 36 | ctctgcactcatggatcttttctttcataggttggatctcgactacagav | chr16 | 15892415 | 15892612 |
| MYH11 | MYH11_70 | TTCCTGGCAAGAACTGCAGACA | ACATGTACAAGGGCAAGAAGAGG | 162 | 59 | TTCCTGGCAAGAACTGCAGACAAGCAGGACAGGAGC | chr16 | 15917034 | 15917195 |
| MYH11 | MYH11_71 | CTGCGATGGCGTAGATGTGAG | CCTGGAGGAGGTCTGGAAGTAA | 172 | 55 | CTGCGATGGCGTAGATGTGAGGNGGCATCTCGTGCC | chr16 | 15917139 | 15917310 |
| MYH11 | MYH11_72 | cagccCTCCCAACACATTTCTAA | AAGATGAACCCACCCAAGTTCTC | 192 | 53 | cagccCTCCCAACACATTTCTAATGCCTACTTTCCTTAT | chr16 | 15931687 | 15931878 |
| MYH11 | MYH11_73 | CCGCTCCCTCAGGTTGTGTA | GCAGCCAGCATTAAGGAGGAG | 186 | 57 | CCGCTCCCTCAGGTTGTGTAGCACGGAGGCTTCGTTC | chr16 | 15931786 | 15931971 |
| MYH11 | MYH11_74 | TCTGGATGTCATCTTTCCCAACC | ACAAAAACTTCATCAACAGCCCAG | 183 | 57 | TCTGGATGTCATCTTTCCCAACCGTGACCTTCTTGCCA | chr16 | 15931878 | 15932060 |
| MYH11 | MYH11_75 | TCATCCCCCTTCTCCTCCTTAAT | TTATTCCACAGGGGACCAACAAG | 198 | 57 | TCATCCCCCTTCTCCTCCTTAATGCTGGCTGCCTCRAA | chr16 | 15931940 | 15932137 |
| MYLK | MYLK_1 | TGACTTAGAAACTGCTTTTCTCTGG | ATTAGTGATGTTTGCGGGGATGA | 173 | 49 | TGACTTAGAAACTGCTTTTCTCTGGCTTTGTTTCACTC | chr3 | 123332920 | 123333092 |
| MYLK | MYLK_1_1 | CACCTAGAAAGACACACAGCTCC | TGCAGTTCAGAGCAACTTCAGG | 197 | 53 | CACCTAGAAAGACACACAGCTCCCCTCTCTGCAGCCT | chr3 | 123550300 | 123550496 |
| MYLK | MYLK_1_2 | TCTGTTGTTTGTTGTGGCAACTG | CGTGTCTGTCTCTGATTTGGCTT | 162 | 57 | TCTGTTGTTTGTTGTGGCAACTGGGCCAGTGGGACA | chr3 | 123550405 | 123550566 |
| MYLK | MYLK_2 | CCTTCCTCCATCGTTTCCACAAT | AGATGACCAGTCAATCAGGGAGT | 183 | 51 | CCTTCCTCCATCGTTTCCACAATGWGCTCTGCTGTGC | chr3 | 123332983 | 123333165 |
| MYLK | MYLK_2_1 | TGAAAGGAAGTGCTTTTTCCTGA | TTTCTTTGATTTGTGTATTAGGAAGGATT | 186 | 29 | TGAAAGGAAGTGCTTTTTCCTGAGAAACTATAAAGTC | chr3 | 123595300 | 123595485 |
| MYLK | MYLK_2_2 | TGCTATTACCTTTATTTTTTCTCTTCAGC | tgTCAACCTGATTTGATGTTTCACT | 132 | 30 | TGCTATTACCTTTATTTTTTCTCTTCAGCTGGCCCRAA | chr3 | 123595397 | 123595528 |
| MYLK | MYLK_3 | CAGGTGTACTTGGCATCGTCATC | CTGCAACTTGTGTTCTCTCCCTG | 176 | 51 | CAGGTGTACTTGGCATCGTCATCCCCGCAAACATCAC | chr3 | 123333052 | 123333227 |

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|---|---|---|---|---|---|---|---|---|---|
| MYLK | MYLK_4 | CTACCATCCAGCCACACCCTATT | AAGATGTGTCCCAAGCTTTCCTT | 186 | 44 | CTACCATCCAGCCACACCCTATTCATGGTGAAGAGAA | chr3 | 123337432 | 123337617 |
| MYLK | MYLK_5 | AGCACAGCTACAACTTACCTTCA | TGACCTGGTCTTCTTCTCTGTCT | 178 | 43 | AGCACAGCTACAACTTACCTTCAATCTTGCAGTCAAA | chr3 | 123337468 | 123337645 |
| MYLK | MYLK_6 | ACCAACCAAAACCTCAAAATGCC | CCTCTATGGCAATGATCTCAGGG | 172 | 51 | ACCAACCAAAACCTCAAAATGCCCCTTTGTTCCCCAG | chr3 | 123338975 | 123339146 |
| MYLK | MYLK_7 | ACTCCTCCTTACCTTCAGATTCTAGT | CAGCTGGAACCAGGGACAAC | 194 | 52 | ACTCCTCCTTACCTTCAGATTCTAGTTTTTCTGCATTG | chr3 | 123339042 | 123339235 |
| MYLK | MYLK_8 | TGAAAGTGGCTTGAACAACACAA | CAGCATCCATGGCTAATGAAAGA | 162 | 46 | TGAAAGTGGCTTGAACAACACAAATATGAGGGGCAA | chr3 | 123345599 | 123345760 |
| MYLK | MYLK_9 | GACCCTCTCATTACCTGCCATTT | TCCTCCTGCTCAAAAATCTCCTG | 178 | 50 | GACCCTCTCATTACCTGCCATTTCCTTCTTGCCATGTA | chr3 | 123345651 | 123345828 |
| MYLK | MYLK_10 | AAAGGAATCCCCCTTTGCTTCC | GACAACGATAACGAAACCTTGGC | 198 | 49 | AAAGGAATCCCCCTTTGCTTCCCAACACAGGGCAGG | chr3 | 123348248 | 123348445 |
| MYLK | MYLK_11 | CTGATGAAATCCTTGGCATCGTC | CTAGCCACACCTGCTGTCC | 165 | 54 | CTGATGAAATCCTTGGCATCGTCGGAGATCTCATCGA | chr3 | 123348345 | 123348509 |
| MYLK | MYLK_12 | GACCCTCCTGTGGAACCCTC | GTCTCTGAAGGTCCTCTTTGGC | 194 | 58 | GACCCTCCTGTGGAACCCTCAGCCCCCACCCACTGGT | chr3 | 123356838 | 123357031 |
| MYLK | MYLK_13 | ATGTAGCAGATGACCCCGATG | TCCGTGATGTGCTGGCAATTTAT | 165 | 52 | ATGTAGCAGATGACCCCGATGCTCCACATGTCTGTGC | chr3 | 123356921 | 123357085 |
| MYLK | MYLK_14 | CACTCAGTGTGAGAGGAAACGG | GGAGTACATCCACAAGCAGGG | 189 | 56 | CACTCAGTGTGAGAGGAAACGGCCAGTGCAATACAC | chr3 | 123359064 | 123359252 |
| MYLK | MYLK_15 | CCAAAGTCGATGAGCTTGATCCT | TCATTGACGAGGACTTTGAGCTG | 172 | 54 | CCAAAGTCGATGAGCTTGATCCTGGTGCCCGTCTTGT | chr3 | 123359151 | 123359322 |
| MYLK | MYLK_16 | GATGCCCTGCTTGTGGATGTA | CATGAGCCTGTGGCCTGAC | 167 | 57 | GATGCCCTGCTTGTGGATGTACTCCACTCCCTCCGAG | chr3 | 123359228 | 123359394 |
| MYLK | MYLK_17 | CAGTAGGGGAGACACGTTTGG | AGGCATATTCAGCAAAAGAGAAAGA | 197 | 54 | CAGTAGGGGAGACACGTTTGGGGGCTCCCTGTGGTC | chr3 | 123366007 | 123366203 |
| MYLK | MYLK_18 | ACACTGGACCAGCTTAGGGT | GGCTAAATGTGGCTTTTCTCTCC | 198 | 46 | ACACTGGACCAGCTTAGGGTGGTGGAGGCAGTTCAT | chr3 | 123366118 | 123366315 |
| MYLK | MYLK_19 | TGAGGCACTGAATCTAACTGTG | ACCAACCCTGACCTGTGC | 196 | 51 | TGAGGCACTGAATCTAACTGTGAGACCCGCACCACCC | chr3 | 123367741 | 123367936 |
| MYLK | MYLK_20 | TAATCAACCTCGGGCTCCTTCTC | CTGTGTCCTCTCTGTCCTTCCTT | 191 | 59 | TAATCAACCTCGGGCTCCTTCTCATCTGTGGGGCACA | chr3 | 123367887 | 123368077 |
| MYLK | MYLK_21 | AAGGTCAGTCACGCACATTTGTT | AGCACCTCTTTCAACGTCCAG | 187 | 49 | AAGGTCAGTCACGCACATTTGTTTCAAGCYACTGATG | chr3 | 123375919 | 123376105 |
| MYLK | MYLK_22 | GGCTTGGCTCACTGGTT | GTCCTGGTATGGCTCCTCAT | 200 | 54 | GGCTTGGCTCACTGGTTCCAYACACGTTGATTGCACG | chr3 | 123376012 | 123376211 |
| MYLK | MYLK_23 | TAGTTCCTTCCACGTCTTGTTGG | TCTGGAAAGTGTGGGTGATGTTG | 198 | 54 | TAGTTCCTTCCACGTCTTGTTGGCTGAGTCCCAGATC | chr3 | 123376118 | 123376315 |
| MYLK | MYLK_24 | CCTGAGGCCCACGTATCTTG | ATGGCAGCAAGCTCACCATC | 195 | 65 | CCTGAGGCCCACGTATCTTGCCTGGGGGCTCCCTGCC | chr3 | 123382871 | 123383065 |
| MYLK | MYLK_25 | GCTGCCCAGCTTGTTCTCC | GAGCCCCCTTCCTTTCCTAGC | 189 | 62 | GCTGCCCAGCTTGTTCTCCACCAGCAGTGTGTAGCAG | chr3 | 123382983 | 123383171 |
| MYLK | MYLK_26 | GGTCCAAAGGCTGTACGGATTATT | CCTCAGATCATCCAGTTCCCTGA | 182 | 57 | GGTCCAAAGGCTGTACGGATTATTCCCAGCACCCCCA | chr3 | 123385004 | 123385185 |
| MYLK | MYLK_27 | GCTTTCGGAACTTCATCCAGGTA | TGATCAGAATGCCTGAGACCCTT | 183 | 55 | GCTTTCGGAACTTCATCCAGGTACAGGTGATGGGCT | chr3 | 123385068 | 123385250 |
| MYLK | MYLK_28 | CAAAACCCCCATGGTAGATGACT | GCCAGTGGACAAGACTGCAT | 198 | 47 | CAAAACCCCCATGGTAGATGACTTCTTTGACCCCAGA | chr3 | 123385928 | 123386125 |
| MYLK | MYLK_29 | GCAAGAGTGAGTGACCAGAAAGT | CAGCCAGTGAGAACACCAAGG | 186 | 61 | GCAAGAGTGAGTGACCAGAAAGTGGGGGCTCTGAG | chr3 | 123400966 | 123401151 |
| MYLK | MYLK_30 | AGTACTCACTCTCAGTTCCTAGC | GAGTTTGGCTGAGGTGGGATTTT | 188 | 51 | AGTACTCACTCTCAGTTCCTAGCACGGGAGGAAGAG | chr3 | 123401062 | 123401249 |
| MYLK | MYLK_31 | CTGACAGGCAAGGTATGGTAAGG | GCCTGAGGACAGAGGCTTATACA | 170 | 59 | CTGACAGGCAAGGTATGGTAAGGAAGGSAGGGGCT | chr3 | 123411495 | 123411664 |
| MYLK | MYLK_32 | GAGAAATGGGACCCCTGTGTATG | TGGTTCACTCCACAATTCTTCCT | 198 | 58 | GAGAAATGGGACCCCTGTGTATGGGTGGCGGCGAT | chr3 | 123411530 | 123411727 |
| MYLK | MYLK_33 | GAGACCAACGCTCCATGAGCTA | CAAGAAGCTGCTGCTCCAGT | 188 | 57 | GAGACCAACGCTCCATGAGCTAGGAGTGGCCCTGGT | chr3 | 123418792 | 123418979 |
| MYLK | MYLK_34 | TTCAGCGTCCAGATGATGGTG | ATGATGTGAACTGCAAGAGAGGC | 184 | 55 | TTCAGCGTCCAGATGATGGTGGCTGGGGGGTCAGAA | chr3 | 123418914 | 123419097 |
| MYLK | MYLK_35 | CTTCTTGCCCTCTGCCACAT | CCAAGCCTGATGAGAACCTGAAA | 185 | 48 | CTTCTTGCCCTCTGCCACATGAACATCTTGCAGCTTCT | chr3 | 123418973 | 123419157 |
| MYLK | MYLK_36 | TCACATCATTCTTAACGTCTTTCTTGA | GTTCCAAGCCCCTGAGCAAT | 198 | 54 | TCACATCATTCTTAACGTCTTTCTTGAGNNSTNNNNT | chr3 | 123419089 | 123419286 |
| MYLK | MYLK_37 | CATTGGCTTCAGGGTCTCAGC | CCTGCCACCCCGGATTTTC | 189 | 58 | CATTGGCTTCAGGGTCTCAGCAGGCTTGGCGTTGCCC | chr3 | 123419201 | 123419389 |
| MYLK | MYLK_38 | CTTGGCATTCAGGGTCTCGG | GAAGAGAGGAAGGTGCACAGC | 198 | 58 | CTTGGCATTCAGGGTCTCGGCACTGCTGCTGCCATTC | chr3 | 123419297 | 123419494 |
| MYLK | MYLK_39 | CGGTGGCACCTTCTCAGG | CAAAGACCCTATCGGAAGACG | 200 | 56 | CGGTGGCACCTTCTCAGGCACGGGGGTCTTGGRAGT | chr3 | 123419396 | 123419595 |
| MYLK | MYLK_40 | CTGTGCACCTTCCTCTCTTCCTC | GGTGGAGCAGCTGGACTTC | 168 | 55 | CTGTGCACCTTCCTCTCTTCCTCAGACACAGTCTTTGG | chr3 | 123419475 | 123419642 |
| MYLK | MYLK_41 | CCGATAGGGTCTTTGTACTCACC | CAGCAAGAGGGCAGGGTTG | 174 | 63 | CCGATAGGGTCTTTGTACTCACCTTCTTSCCCAGGAG | chr3 | 123419581 | 123419754 |
| MYLK | MYLK_42 | GCGCCTCTTCAGCACCC | ACTTTCCTTTTTCCCTACACTGGT | 195 | 63 | GCGCCTCTTCAGCACCCCTCGCACGTCCTCGCCGTCTT | chr3 | 123419687 | 123419881 |

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|---|---|---|---|---|---|---|---|---|---|
| MYLK | MYLK_43 | CCAGGAGGAAGGTGGGGAT | GAGGGCCTCTTGATCTTTATTGA | 171 | 58 | CCAGGAGGAAGGTGGGGATGSGGGCATGGCCTGGA | chr3 | 123420226 | 123420396 |
| MYLK | MYLK_44 | GTTAGGGGAGCTAGGAATTTGGA | ACTGGCTCAGAGATGGCAAAG | 196 | 55 | GTTAGGGGAGCTAGGAATTTGGAGGGAAGGGTTAA | chr3 | 123426538 | 123426733 |
| MYLK | MYLK_45 | TGAACACGTCCTCATTCTGAAGC | CACCCAGCCCTGGTTCATC | 179 | 58 | TGAACACGTCCTCATTCTGAAGCACCTCGAAGTGGCC | chr3 | 123426659 | 123426837 |
| MYLK | MYLK_46 | CTTTGCCATCTCTGAGCCAGT | CTGCCTGCTGAGGGACATC | 189 | 59 | CTTTGCCATCTCTGAGCCAGTGCACGGTAGGAAAGG | chr3 | 123426713 | 123426901 |
| MYLK | MYLK_47 | TTCCTTGCCTCCAAATCACTTTT | AGAGGAACTCAGCACAGCCTT | 198 | 60 | TTCCTTGCCTCCAAATCACTTTTGGAGGGGCTGCAGC | chr3 | 123427468 | 123427665 |
| MYLK | MYLK_48 | CCAGGCCTCGCAGGTGTA | GAGGACCTCCCTAACCAATCCC | 196 | 57 | CCAGGCCTCGCAGGTGTACGTGCCCGTGTCCTCCGG | chr3 | 123427591 | 123427786 |
| MYLK | MYLK_49 | CCCATTGCAACCAAGACCATTTT | AGTAGCAGGAAGAGTGAGTACCT | 189 | 52 | CCCATTGCAACCAAGACCATTTTCATGTTAATCCCNNI | chr3 | 123428544 | 123428732 |
| MYLK | MYLK_50 | GTCATAGTGACCTGGCTTCCATC | GAATGCATGAATGTTCACCCCAC | 168 | 51 | GTCATAGTGACCTGGCTTCCATCCATGACTTTGAGAT | chr3 | 123428617 | 123428784 |
| MYLK | MYLK_51 | CCATTTTCTACAAATGTGCCCTTCC | GAGGACCATGGCACCTACAC | 163 | 57 | CCATTTTCTACAAATGTGCCCTTCCTCCAAAGCARAAC | chr3 | 123440891 | 123441053 |
| MYLK | MYLK_52 | AGGCGCTGCAGGACAC | GAGCCTTCCTGTGCTTCCTC | 163 | 65 | AGGCGCTGCAGGACACCTGCCCCAAGGCATTCTCAG | chr3 | 123440990 | 123441152 |
| MYLK | MYLK_53 | TGGCTCAGAGGGATAAGTGAGAA | TGAAGGACTGCGCTGTTATTGAG | 177 | 60 | TGGCTCAGAGGGATAAGTGAGAATTCAGGCAGCGCC | chr3 | 123444707 | 123444883 |
| MYLK | MYLK_54 | CACCATTCAGCAGCCAAGTGA | GATCTGAGCTGACCTGTCCTTTT | 170 | 59 | CACCATTCAGCAGCCAAGTGATCCGGGGCACTGGGG | chr3 | 123444788 | 123444957 |
| MYLK | MYLK_55 | CCATGAATGGTTGTCCCACAGAG | AGGTTTATGAAGATGCTGGCTCC | 186 | 55 | CCATGAATGGTTGTCCCACAGAGAATGCGGGGTGAC | chr3 | 123451689 | 123451874 |
| MYLK | MYLK_56 | CAGCTGTATGTCCCACTGTCC | GCATAGGGAGCTCACGTTCTTTA | 187 | 56 | CAGCTGTATGTCCCACTGTCCCTGGTCCGGGCTTTCA | chr3 | 123451799 | 123451985 |
| MYLK | MYLK_57 | GGCCACCAAGGGGCTAC | GAGCCAAGATGTTGTGAGCAAG | 194 | 50 | GGCCACCAAGGGGCTACATTTTGGCAATYGGTGACC | chr3 | 123452480 | 123452673 |
| MYLK | MYLK_58 | TTTTCCTTGACCTCCTGGCTTTG | GAAGAGAGGAAGAGGCCAGCTC | 179 | 58 | TTTTCCTTGACCTCCTGGCTTTGGGGCTTGCTCTCAAA | chr3 | 123452560 | 123452738 |
| MYLK | MYLK_59 | TTAGCAGCCTTGCTCACAACATC | GTCCTTCAGAAGACTTCCAGCTC | 191 | 60 | TTAGCAGCCTTGCTCACAACATCTTGGCTCCCCAGGC | chr3 | 123452644 | 123452834 |
| MYLK | MYLK_60 | CTGGCCTCTTCCTCTCTTCTCC | GTCCAAGCTGGAGTCATGCAA | 167 | 59 | CTGGCCTCTTCCTCTCTTCTCCAGAAGGTGATAGGnn | chr3 | 123452720 | 123452886 |
| MYLK | MYLK_61 | GGGTGATGGAGCTGGAAGTC | AGGAGTCGAAGCTGGACA | 198 | 61 | GGGTGATGGAGCTGGAAGTCTTCTGAAGGACCRGRC | chr3 | 123452804 | 123453001 |
| MYLK | MYLK_62 | GGGAGCCACCTCTCTGG | CATTCTATTCTCCCCTCTCCTCAC | 198 | 54 | GGGAGCCACCTCTCTGGGGGCTGGAGCAGTTCTTGC | chr3 | 123452927 | 123453124 |
| MYLK | MYLK_63 | CCAATTCTTCTGCCCCATAAGATGA | CTAACAGTCTTTCCACCCTTCCC | 163 | 44 | CCAATTCTTCTGCCCCATAAGATGATTCAGAAATTCA | chr3 | 123454135 | 123454297 |
| MYLK | MYLK_64 | CAGTGAACAAGCAGCTCCTCTA | CGGCATGCAGGTTCTGGAAA | 194 | 57 | CAGTGAACAAGCAGCTCCTCTAGGAGGGTGCGGCAC | chr3 | 123456147 | 123456340 |
| MYLK | MYLK_65 | CTGACATCGAGGCCTTCCC | TATGACCAAGTTACCCCATTGCC | 179 | 54 | CTGACATCGAGGCCTTCCCCGACCCGTTCACCACCAG | chr3 | 123456243 | 123456421 |
| MYLK | MYLK_66 | CGGGTATGTCTATTAGCAGCATGAG | GGGGAGTGCCCACCAAAG | 194 | 55 | cgggtatgtctattagcagcatgagaacagactaatacaGGMTG | chr3 | 123457670 | 123457863 |
| MYLK | MYLK_67 | GCCGGCCAGTGATCTTG | GATGGTTGAATTGCTGCCTTGTC | 195 | 53 | GCCGGCCAGTGATCTTGCAGGAGAATCGTCCCATCTC | chr3 | 123457770 | 123457964 |
| MYLK | MYLK_68 | CTCAAGTCAGCAGGAAAGCAATC | CACCCCTGCTGTTGAATCTTTTT | 188 | 46 | CTCAAGTCAGCAGGAAAGCAATCCAACCCTTACTCTG | chr3 | 123458742 | 123458929 |
| MYLK | MYLK_69 | GCCTTGGGGTAACTGAGAGC | CCGCTTCCTGCTGGATTG | 200 | 57 | GCCTTGGGGTAACTGAGAGCTCAGCTCCCTCCTGGAC | chr3 | 123471121 | 123471320 |
| MYLK | MYLK_70 | ACAGGTATACTTTCCCCTGTCCT | caggctcttaCCCTTTCTTCTTT | 185 | 57 | ACAGGTATACTTTCCCCTGTCCTCCTCATGGACAGCAT | chr3 | 123471233 | 123471417 |
| MYLK | MYLK_71 | GGCCCCTGCCCATCCTT | CGTCACACATTTCCAAAACCTCC | 191 | 58 | GGCCCCTGCCCATCCTTCCCCACAGCCTCCCCATCCAC | chr3 | 123512473 | 123512663 |
| MYLK | MYLK_72 | CTTACCCGCCCTTCGAACTTG | TTGTCCTCTTCCTTCCTTTTTGC | 198 | 54 | CTTACCCGCCCTTCGAACTTGGCGGTGGCTCCTTCTTT | chr3 | 123512519 | 123512716 |
| SMAD3 | SMAD3_1 | GGCCGAGCTCCCCTCT | CGCCTTCTCGCACCATTTCTC | 189 | 72 | GGCCGAGCTCCCCTCTGCGCCCCCGGCGTCCCGTCGA | chr15 | 67358406 | 67358594 |
| SMAD3 | SMAD3_2 | ATGTCGTCCATCCTGCCTTTC | GATGCACTTGGTGTTGACGTTC | 195 | 59 | ATGTCGTCCATCCTGCCTTTCACTCCCCCGATCGTGAA | chr15 | 67358493 | 67358687 |
| SMAD3 | SMAD3_3 | GCCTGGTCAAGAAACTCAAGAAG | CTCTCTCTCCCTCTTCCCATCTC | 198 | 68 | GCCTGGTCAAGAAACTCAAGAAGACGGGGCAGCTGC | chr15 | 67358602 | 67358799 |
| SMAD3 | SMAD3_4 | GGAAGGGCTGTATTGTCCTTATCA | GGGGAGACGAGTTCAAGAAAGAG | 197 | 56 | GGAAGGGCTGTATTGTCCTTATCATCAGAATCCCTCC | chr15 | 67430295 | 67430491 |
| SMAD3 | SMAD3_5 | CAGAAAGCAAGCACAATCCACAT | TATTGAAGGCGAACTCACACAGC | 194 | 60 | CAGAAAGCAAGCACAATCCACATTTCCCTCTCTTTCTC | chr15 | 67457176 | 67457369 |
| SMAD3 | SMAD3_6 | GGGCTCCCTCATGTCATCTACT | CTGGCACCTGCTGTCCC | 197 | 60 | GGGCTCCCTCATGTCATCTACTGCCGCCTGTGGCGAT | chr15 | 67457270 | 67457466 |
| SMAD3 | SMAD3_7 | GGGACTTTGGTGCTGGTCTG | GGGAAGTTAGTGTTTTCGGGGAT | 162 | 60 | GGGACTTTGGTGCTGGTCTGGCATCGACACTGAGCC | chr15 | 67457529 | 67457690 |
| SMAD3 | SMAD3_8 | CCACGCCACACAGAGATCC | CAGAGATTGGGGCCACAGG | 195 | 64 | CCACGCCACACAGAGATCCCGGCCGAGTTCCCCCCAC | chr15 | 67457611 | 67457805 |
| SMAD3 | SMAD3_9 | TCAGAGCCAAGCTGTGAAGG | GATGAACCCACCAGCTGCTAATC | 187 | 52 | TCAGAGCCAAGCTGTGAAGGCCTTTTAACAGACCAC | chr15 | 67459063 | 67459249 |

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|---|---|---|---|---|---|---|---|---|---|
| SMAD3 | SMAD3_10 | AGTGTTTAGTAACTTGGCTCTCCA | GCCCCCTCCCCACACT | 198 | 53 | AGTGTTTAGTAACTTGGCTCTCCAGGCCAAGAATCTT | chr15 | 67462822 | 67463019 |
| SMAD3 | SMAD3_11 | GAGGGAGCATGGGGCTTG | AATTGGAGGGGTCGGTGAAG | 195 | 61 | GAGGGAGCATGGGGCTTGGGACACCCAATGACCCA( | chr15 | 67473522 | 67473716 |
| SMAD3 | SMAD3_12 | CGCGTCGGGGAGACATT | GGGGAATGGAGCCACCC | 167 | 60 | CGCGTCGGGGAGACATTCCACGCCTCGCAGCCATCC/ | chr15 | 67473647 | 67473813 |
| SMAD3 | SMAD3_13 | TGCTGTTCTGCCTCCTTTGC | CTGGTTACAGTTGGGAGACTGG | 188 | 56 | TGCTGTTCTGCCTCCTTTGCGAGCCTCAGGTGGCCCC, | chr15 | 67476972 | 67477159 |
| SMAD3 | SMAD3_14 | TACTACATCGGAGGGGAGGTCTT | CATGCACTCGGAGAGGGAC | 173 | 59 | TACTACATCGGAGGGGAGGTCTTCGCAGAGTGCCTC, | chr15 | 67477082 | 67477254 |
| SMAD3 | SMAD3_15 | GGACTTGCTTTATCCAGGAGGG | GCACATTCGGGTCAACTGGTAG | 179 | 56 | GGACTTGCTTTATCCAGGAGGGGAGCAACGGACCTG | chr15 | 67479625 | 67479803 |
| SMAD3 | SMAD3_16 | AGTTCGCTGCCCTCCTG | CCAGAGTCACCTGGAGTTGG | 167 | 59 | AGTTCGCTGCCCTCCTGGCCCAGTCGGTCAACCAGGC | chr15 | 67479733 | 67479899 |
| SMAD3 | SMAD3_17 | ACTGTCACCAAAGCAGAAAAAGC | CCATCTGGGTGAGGACCTTG | 182 | 51 | ACTGTCACCAAAGCAGAAAAAGCTTTCTGACTTGTGT | chr15 | 67482658 | 67482839 |
| SMAD3 | SMAD3_18 | ATTTTTTAAGTCCCCCACCCCAC | CTGCCCTCCCCTACCATACTT | 196 | 54 | ATTTTTTAAGTCCCCCACCCCACCCCTTTCCCTATTTCT | chr15 | 67482707 | 67482902 |
| TGFBR1 | TGFBR1_1 | CGTCCTCCGAGCAGTTACAAA | cAGCACGAGGAGGAGCAG | 186 | 77 | CGTCCTCCGAGCAGTTACAAAgggccggagcgaggccgccg | chr9 | 101867353 | 101867538 |
| TGFBR1 | TGFBR1_2 | CGGCGGGACCATGGAG | cATGTTTGAGAAAGAGCAGGAGC | 193 | 76 | CGGCGGGACCATGGAGGCGGCGGTCGCTGCTCCGCC( | chr9 | 101867478 | 101867670 |
| TGFBR1 | TGFBR1_3 | TGGATAATTTCAAACTGTTAACCTTGAG | TGCTGTTGTGTATAACTTTGTCTGTG | 170 | 38 | TGGATAATTTCAAACTGTTAACCTTGAGATTTTTTCTA | chr9 | 101891078 | 101891247 |
| TGFBR1 | TGFBR1_4 | GTTACAGTGTTTCTGCCACCTCT | TGCACATACAAACGGCCTATCTC | 163 | 42 | GTTACAGTGTTTCTGCCACCTCTGTACAAAAGACAAT | chr9 | 101891138 | 101891300 |
| TGFBR1 | TGFBR1_5 | ACACAACAGCATGTGTATAGCTGA | GTATGAAGAGTTTTTCTTGTAGTATCTAGG | 198 | 36 | ACACAACAGCATGTGTATAGCTGAAATTGACTTAATT | chr9 | 101891237 | 101891434 |
| TGFBR1 | TGFBR1_6 | GTTGCCACCTACAGTGTTTTTGT | ATTTGGCACTCGATGGTGAATGA | 198 | 47 | GTTGCCACCTACAGTGTTTTTGTCGTTGTTGATGTTTA | chr9 | 101894730 | 101894927 |
| TGFBR1 | TGFBR1_7 | TGCATCTCACTCATGTTGATGGT | GATGTCTTAGGAAAAAGGAGAAACAA | 198 | 41 | TGCATCTCACTCATGTTGATGGTCTATAYCTGCCACA/ | chr9 | 101894859 | 101895056 |
| TGFBR1 | TGFBR1_8 | ATCAGTTTTCTGGGTCACTCATT | CCACTTTCCTCTCCAAACTTCTCC | 192 | 36 | ATCAGTTTTCTGGGTCACTCATTAGTGCCTATCATGA1 | chr9 | 101900047 | 101900238 |
| TGFBR1 | TGFBR1_9 | TTCAGAGAACAATTGCGAGAACT | TCCCAGGATGTTTTCATGACGTA | 194 | 42 | TTCAGAGAACAATTGCGAGAACTATTGTGTTACAAG/ | chr9 | 101900156 | 101900349 |
| TGFBR1 | TGFBR1_10 | CATTGGCAAAGGTCGATTTGGAG | ACAGACCTTTATTGTCTGCTGCT | 182 | 43 | CATTGGCAAAGGTCGATTTGGAGAAGTTTGGAGAGC | chr9 | 101900196 | 101900377 |
| TGFBR1 | TGFBR1_11 | ATGTTACGTCATGAAAACATCCTG | TGTATTCGACTTAATGGGTCTAATCTAC | 187 | 34 | ATGTTACGTCATGAAAACATCCTGGGATTTATAGCAC | chr9 | 101900323 | 101900509 |
| TGFBR1 | TGFBR1_12 | CCATTGAACAAATAAATCATAAATGGTCTGC | AGCAAGTTTTATCATTCCTTCCACA | 176 | 37 | CCATTGAACAAATAAATCATAAATGGTCTGCAGCCCA | chr9 | 101904755 | 101904930 |
| TGFBR1 | TGFBR1_13 | AGACAATGGTACTTGGACTCAGC | TGGGTACCAACAATCTCCATGTG | 168 | 44 | AGACAATGGTACTTGGACTCAGCTCTGGTTGGTGTC/ | chr9 | 101904816 | 101904983 |
| TGFBR1 | TGFBR1_14 | AGGAATGATAAAACTTGCTCTGTCCA | AAAGCTTAAATAATAGAACTGCTTATAGAATTACC | 108 | 41 | AGGAATGATAAAACTTGCTCTGTCCAYGGCGAGCGG | chr9 | 101904912 | 101905019 |
| TGFBR1 | TGFBR1_15 | TGGGAGAAGAGACTTTTGAACCTAA | AATCATGTCTTACTGCCAGTCCT | 191 | 36 | TGGGAGAAGAGACTTTTGAACCTAAAGATGTGAGTT | chr9 | 101906928 | 101907118 |
| TGFBR1 | TGFBR1_16 | TGATTCTTTAGGAAAGCCAGCCAT | GTTCCCACTCTGTGGTTTGGA | 162 | 40 | TGATTCTTTAGGAAAGCCAGCCATTGCTCATAGAGAT | chr9 | 101907003 | 101907164 |
| TGFBR1 | TGFBR1_17 | ACATGATTCAGCCACAGATACCATT | CCATGAGATCTTCTTACCTGTTGG | 198 | 34 | ACATGATTCAGCCACAGATACCATTGATATTGCTCCA, | chr9 | 101907111 | 101907308 |
| TGFBR1 | TGFBR1_18 | TGTATAAAGAAATGTCTGAAAGGAGGT | TCCCAGAATACTAAGCCCATTGC | 186 | 36 | TGTATAAAGAAATGTCTGAAAGGAGGTTCATCCAAA | chr9 | 101908680 | 101908865 |
| TGFBR1 | TGFBR1_19 | CCCCTGAAGTTCTCGATGATTCC | ACAATTCTTGAACAACTTCTGCTC | 176 | 41 | CCCCTGAAGTTCTCGATGATTCCATAAATATGAAACA | chr9 | 101908775 | 101908950 |
| TGFBR1 | TGFBR1_20 | TGCCTTGGCATTAGCTGAATAAA | GCCATCTGTTTGGGATATTTGGC | 178 | 34 | TGCCTTGGCATTAGCTGAATAAATTCATCAAAATTTA, | chr9 | 101909878 | 101910055 |
| TGFBR1 | TGFBR1_21 | TCATGAAGATTACCAACTGCCTT | TAGAAAATTGCCTAATATCAAAAAGAAATACTCA | 162 | 36 | TCATGAAGATTACCAACTGCCTTATTATGATCTTGTAC( | chr9 | 101909940 | 101910101 |
| TGFBR1 | TGFBR1_22 | ACAGAAGTTAAGGCCAAATATCCCA | ACATTGGTTTGACTGCTATGAAAAA | 175 | 31 | ACAGAAGTTAAGGCCAAATATCCCAAACAGATGGCA | chr9 | 101910021 | 101910195 |
| TGFBR1 | TGFBR1_23 | TCTTATCCAGACCAATGGAAAATGG | ATGCCTTCCTGTTGACTGAGTTG | 178 | 37 | TCTTATCCAGACCAATGGAAAATGGTGCATGCattaat | chr9 | 101911400 | 101911577 |
| TGFBR1 | TGFBR1_24 | GTATGCCAATGGAGCAGCTAGG | ATATCCTTCTGTTCCCTCTCAGT | 192 | 42 | GTATGCCAATGGAGCAGCTAGGCTTACAGCATTGCG | chr9 | 101911500 | 101911691 |
| TGFBR1 | TGFBR1_25 | TATCGCAACTCAGTCAACAGGAA | ATTACACTGCTGCAAAAGGAAGC | 166 | 41 | TATCGCAACTCAGTCAACAGGAAGGCATCAAAATGT/ | chr9 | 101911550 | 101911715 |
| TGFBR2 | TGFBR2_1 | TATGACGAGCAGCGGGGTC | GTCAAGCGCAGCGGAGAG | 193 | 71 | TATGACGAGCAGCGGGGTCTGCCATGGGTCGGGGG | chr3 | 30648353 | 30648545 |
| TGFBR2 | TGFBR2_2 | AAAAACAGCTCTCTGAGATGGATA | ATTAAGCAGTGAGGGAGCATGAC | 185 | 36 | aaaaacagctctctgagatggatataattatcctgttttacagatgtgg | chr3 | 30664648 | 30664832 |
| TGFBR2 | TGFBR2_3 | AACATCTTCAGGAATTCATTGGC | CTCATGCAGGATTTCTGGTTGTC | 186 | 40 | AACATCTTCAGGAATTCATTGGCAGGCTGCCTGGCAC( | chr3 | 30686165 | 30686350 |
| TGFBR2 | TGFBR2_4 | GTGCAGTCAAGTTTCCACAACTG | ACATTATGTAAAAAGGGGAAAAGAAAGA | 189 | 42 | GTGCAGTCAAGTTTCCACAACTGTGTAAATTTTGTGA | chr3 | 30686272 | 30686460 |
| TGFBR2 | TGFBR2_5 | CCCTCGCTTCCAATGAATCTCTT | GCACTCATCAGAGCTACAGGAAC | 197 | 44 | CCCTCGCTTCCAATGAATCTCTTCACTCTAGGAGAAA( | chr3 | 30691731 | 30691927 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| TGFBR2 | TGFBR2_6 | ACTAGAGACAGTTTGCCATGACC | GGTCCCACACCCTTAAGAGAAGA | 198 | 44 | ACTAGAGACAGTTTGCCATGACCCCAAGCTCCCCTAC | chr3 | 30691786 | 30691983 |
| TGFBR2 | TGFBR2_7 | CCCACTTCCTGACAGTACTTACC | TGATGACAGATATGGCAACTCCC | 163 | 47 | CCCACTTCCTGACAGTACTTACCTACCACATCCAACTC | chr3 | 30713063 | 30713225 |
| TGFBR2 | TGFBR2_8 | AGTCATATTTCAAGTGACAGGCATCA | CTGATGTCAGAGCGGTCATCTTC | 198 | 52 | AGTCATATTTCAAGTGACAGGCATCAGCCTCCTGCCA | chr3 | 30713161 | 30713358 |
| TGFBR2 | TGFBR2_9 | CAACCTGGGAAACCGGCAA | TATAGACCTCAGCAAAGCGACCT | 183 | 56 | CAACCTGGGAAACCGGCAAGACGCGGAAGCTCATGC | chr3 | 30713271 | 30713453 |
| TGFBR2 | TGFBR2_10 | CCAACAACATCAACCACAACACA | GTCCTTCTCTGTCTTCCAAGAGG | 182 | 51 | CCAACAACATCAACCACAACACAGAGCTGCTGCCCAT | chr3 | 30713370 | 30713551 |
| TGFBR2 | TGFBR2_11 | TTCAGAGCAGTTTGAGACAGTGG | CGGTGATCAGCCAGTATTGTTTC | 176 | 48 | TTCAGAGCAGTTTGAGACAGTGGCAGTCAAGATCTT | chr3 | 30713476 | 30713651 |
| TGFBR2 | TGFBR2_12 | AGCATGAGAACATACTCCAGTTCC | GATCACTGTGGAGGTGAGCAATC | 195 | 58 | AGCATGAGAACATACTCCAGTTCCYGACGGCTGAGG | chr3 | 30713574 | 30713768 |
| TGFBR2 | TGFBR2_13 | GACGCGGCATGTCATCA | CAGGGAAAGCCCAAAGTCACA | 196 | 59 | GACGCGGCATGTCATCAGCTGGGAGGACCTGCGCAA | chr3 | 30713686 | 30713881 |
| TGFBR2 | TGFBR2_14 | TGTGGGAGGCCCAAGAT | GAGGCCAGGCTCAAGGTAAA | 200 | 54 | TGTGGGAGGCCCAAGATRCCCATCGTGCACAGGGAC | chr3 | 30713777 | 30713976 |
| TGFBR2 | TGFBR2_15 | CAGGGGCCACCATCAGCTATATT | ACCAGAGCCATGGAGTAGACATC | 187 | 45 | CAGGGGCCACCATCAGCTATATTGTGAAAATAAAAA | chr3 | 30715514 | 30715700 |
| TGFBR2 | TGFBR2_16 | TGTCTGTTTTTGCTATAGGTGGGA | ACCACTACACAATGATGCTGGTC | 192 | 48 | TGTCTGTTTTTGCTATAGGTGGGAACTGCRAGATACA | chr3 | 30715579 | 30715770 |
| TGFBR2 | TGFBR2_17 | GCATCTCACCATGCTCATTTCCT | CGATCTCTCAACACGTTGTCCTT | 164 | 49 | GCATCTCACCATGCTCATTTCCTTTGGCTGCACATGCC | chr3 | 30729800 | 30729963 |
| TGFBR2 | TGFBR2_18 | GTGTTTGCTGGCTTTCTTCACAG | GCAACTTGGTTGAATCTTACTGACC | 198 | 48 | GTGTTTGCTGGCTTTCTTCACAGAAGTAAAAGATTAT | chr3 | 30729853 | 30730050 |
| TGFBR2 | TGFBR2_19 | CAAGGTCAGCAGGCCACC | GCCTGTCCAGATGCTCCAG | 191 | 60 | CAAGGTCAGCAGGCCACCTTGCCTTCCGCGGAGCCC | chr3 | 30732836 | 30733026 |
| TGFBR2 | TGFBR2_20 | CTGGGACCACGACCCAGAG | GGGCAGCCTCTTTGGACA | 186 | 61 | CTGGGACCACGACCCAGAGGCCCGTCTCACAGCCCA | chr3 | 30732947 | 30733132 |

Genomic co-ordinates based on GRCh37/hg19 human reference sequence

**Table S3** Transcript IDs used

| Gene | Refgene | ENSGene |
|---|---|---|
| *COL1A1* | NM_000088 | ENSG00000108821 |
| *COL1A2* | NM_000089 | ENSG00000164692 |
| *COL3A1* | NM_000090 | ENSG00000168542 |
| *COL5A1* | NM_000093 | ENSG00000130635 |
| *COL5A2* | NM_000393 | ENSG00000204262 |
| *ACTA2* | NM_001141945 | ENSG00000107796 |
| *FBN1* | NM_000138 | ENSG00000166147 |
| *MYH11* | NM_002474 | ENSG00000133392 |
| *MYLK* | NM_053031 | ENSG00000065534 |
| *SMAD3* | NM_005902 | ENSG00000166949 |
| *TGFBR1* | NM_001130916 | ENSG00000106799 |
| *TGFBR2* | NM_001024847 | ENSG00000163513 |

Supplementary (Appendix, online only material, etc.)

**Table S4** Detailed phenotypic and genetic background of cases with pathogenic variants and variants of unknown significance (VUS)

| Patient ID | Variants identified by NGS | | Genetic testing by previous Sanger sequencing *[a]* | | | | Age (yrs) | Sex | Initial clinical diagnosis | Phenotype details | No. relatives affected *[b]* | Affected mut.positive /mut.negative *[b]* | Beighton score (0-9) | Villefranche criteria - No.major criteria(No. minor criteria) | | | | | Ghent *[c]* | Signs OI *[d]* | Biochem *[e]* | LM *[f]* | EM *[g]* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Gene | Variant type | *COL1A1 /COL1A2* | *COL3A1* | *COL5A1 /COL5A2* | Other Genes | | | | | | | | Classical | Vascular | Hypermob | Kyphoscol | Other EDS | | | | | |
| 31 | *COL5A1* | Pathogenic | | | 1 | | 27 | M | Classical | | 1 | | 7 | 3(3) | | 1(0) | | | | | | + | ++ |
| 49 | *COL3A1* | VUS | | | | | 19 | M | Classical | | 1 | 1 | 9 | 3(3) | | 2(0) | | | | | | | |
| 62 | *COL5A2* | Pathogenic | | | 1 | | 33 | F | Classical | | 1 | 1 | 8 | 3(3) | | | | | 4 | | | - | ++ |
| 429 | *COL5A1* | Pathogenic | | | 1 | | 39 | M | Classical | Thin skin over chest & spine, hypermobile, iliac artery aneurysm and rupture | 1 | | 4 | 2(4) | 3(2) | | | | 1 | | Normal | + | ++ |
| 581 | *COL5A1* | Pathogenic | | | 1 | | 42 | M | Classical | | 1 | 1 | 7 | 2(3) | 0(1) | | | | | | | + | ++ |
| 582 | *COL5A1* | Pathogenic | | | 1 | | 56 | M | Classical | | | | 9 | 1(1) | 0(1) | 2(0) | | | | | Col V | + | ++ |
| 627 | *COL5A1* | Pathogenic | | | 1 | | 78 | M | Classical | Loose fragile skin, atypical for Classical EDS | 0 | | | 3(1) | | | | | | | Normal | | ++ |
| 1129 | *COL5A1* | Pathogenic | | | 1 | | 33 | F | Classical | Joint hypermobility, fragile skin, Varicose veins | 4 | 1 | | 2(4) | 0(1) | | | | | | | | + |
| 636* | *COL3A1 COL5A2* | Pathogenic VUS | | | 1 | *TNXB*: 0 | 21 | M | Classical | Hyperextensible skin, generalised hypermobility including marked distal hypermobility, facies suggestive of Classical EDS, no signs of Vascular EDS | | 0 | 8 | 2(1) | 0(1) | 2(0) | | | 3 | | Normal | + | + |
| 67 | | | | | | *TNXB*: 1 | 33 | M | Classical / Hypermobility overlap | Hyperextensible skin, hypermobility and anal prolapse | 3 | 1 | | 2(4) | | 2(1) | | | 1 | | | - | + |
| 417 | *COL3A1* | Pathogenic | | 1 | | | 31 | M | Classical / Hypermobility / Vascular overlap | Widened atrophic scars, bruisability and friability of skin, marked generalised hypermobility, normal facies, history of recurrent colonic perforations | 1 | | 6 | 2(0) | 1(2) | 1(0) | | | 1 | | Col III | + | + |
| 671 | *COL5A2* | VUS | | | | *PLOD1*: 0 | 45 | F | Classical / Hypermobility overlap | | 3 | 1 | 7 | 2(4) | 1(0) | 2(1) | 1(1) | | 2 | | | - | |
| 37 | *COL3A1* | Pathogenic | | 1 | | | 15 | M | Vascular | Popliteal artery rupture | 6 | | 6 | 0(1) | 3(0) | 2(1) | | | | | Col III | + | + |
| 46 | *COL3A1* | Pathogenic | | 1 | | | 42 | F | Vascular | Vascular EDS facies and aortic rupture | 0 | | 0 | | 3(1) | | | | | | Col III | | + |
| 76 | *COL3A1* | Pathogenic | | 1 | | | 26 | F | Vascular | Spontaneous colon perforation | 0 | | 9 | | 3(2) | 2(2) | | | | | Col III | + | + |
| 384 | *COL1A1* | VUS | 1 | 0 | | *FBN1*: 0 *TGFBR1:* 0 *TGFBR2*: 0 | 42 | F | Vascular | Acrogeria suggestive of vascular EDS; Ascending aortic aneurysm | 2 | | 0 | 1(1) | 3(3) | | | | 0 | | Col III | - | - |
| 405 | *COL3A1* | Pathogenic | | 1 | | | 7 | M | Vascular | Acrogeria & easy bruising | 3 | | | | 3(2) | | | | | | | | |
| 443 | *COL3A1* | Pathogenic | | 1 | | | 44 | F | Vascular | | 2 | 1 | | 1(0) | 3(3) | 1(0) | | | | | | | |
| 448 | *COL3A1* | Pathogenic | | 1 | | | 26 | F | Vascular | Typical acrogeric Vascular EDS | 1 | | 5 | | 2(3) | | | | | | Col III | + | - |
| 483 | *COL3A1* | Pathogenic | | 1 | | | 39 | M | Vascular | Spontaneous colon perforation and positive family history of vascular EDS | 1 | 1 | | | 3(4) | | | | 5 | | | + | + |
| 733 | *COL3A1* | Pathogenic | | 1 | | | 33 | M | Vascular | Spontaneous intra-abdominal haemorrhage | 2 | 2 | | 0(1) | 3(3) | | | | | | | | |
| 1125 | | | | | | *FBN2*: 1 | 38 | M | Vascular | | 1 | 1 | | | | | | | | | Normal | | |
| 444* | *COL1A1* | VUS | | | | CNV ¶ | 29 | M | Vascular | varicose veins, small joint hypermobility, mildly thin and hyperextensible skin, learning difficulties | 0 | 0/0 | 0 | 0(0) | 0(2) | 0(1) | | | 2 | | Col III | - | - |
| 42 | *COL3A1* | Pathogenic | | 1 | | | 38 | F | Vascular / Hypermobility overlap | | 6 | 1/3 Δ | 4 | 0(2) | 1(1) | 0(1) | | | 1 | 1-a | Col III (mild) | (+) | + |
| 765 | *COL3A1* | Pathogenic | | 1 | | | 6 | F | Vascular/ Hypermobility overlap | Subependymal intracerebral haemorrhage at birth, Hypermobility, easy bruising | 1 | | 9 | | 3(0) | 1(1) | | | | 1-a | | | |
| 1088 | *COL5A1* | Pathogenic | | | | | 40 | M | Vascular/ Classical overlap | | 0 | | 3 | 2(0) | 2(2) | | | | 2 | | | | |
| 66* | *FBN1; COL5A1* | Pathogenic; VUS | | 0 | | *FBN1*: 1 | 55 | M | Other HDCT with vascular phenotype | Hypermobility / non-Marfan fibrinillopathy (Ghent =1), short stature, ectopia lentis, Aortic & Mitral valve surgery (aortic dilatation, MV prolapse). | 3 | | | 1(0) | | 1(0) | | | 1 | | | - | - |
| 378 | *FBN1* | Pathogenic | | 0 | | *SMAD3*:0 *TGFBR1*:0 *TGFBR2*:0 | 42 | F | Other HDCT with vascular phenotype | Hypermobility, Carotid artery dissection, early onset osteoarthritis | 1 | | | 0(1) | 1(0) | 1(2) | | | 0 | | | | |
| 420 | *COL3A1* | Pathogenic | | 1 | | | 27 | F | Vascular/ Classical overlap | Vascular EDS facies (prominent eyes, small ear lobes) with hyper-extensible skin and extensive hypermobilility. Haemothorax. | 1 | | 9 | 3(2) | 3(1) | 2(0) | | | | | | | + |
| 34 | *COL5A1* | VUS | | 0 | | | 36 | F | Hypermobility / BJHS | Benign connective tissue phenotype with carotid(cervical) artery dissection | ł (both sides of family) | | 3 | -mild(; | 1(0) | | | | | | | - | - |
| 475 | *TGFBR1* | VUS | 0 | 0 | | | 33 | F | Other HDCT | Hypermobility, soft skin, multiple fractures, mild blue sclerae, systolic murmur | 3 | | 7 | 0(3) | | 2(1) | | | | 2-a. b | | - | - |
| 478 | *COL1A1* | VUS | | 0 | 0 | | 41 | F | Hypermobility / BJHS | | 3 | | 6 | | | 1(3) | | | 0 | | Col III | - | + |

| | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 538 | | | | 0 | | *FLNA*: 1 | 23 | F | Hypermobility / BJHS | Hypermobility, periventricular nodular heterotopia (FLNA mutation not segregating with EDS signs) | 3 | | 0(*FLNA*) | 7 | 0(1) | 1(0) | 1(1) | | | 1 | | | | - | - |
| 558 | *COL1A2* | VUS | | | | | 22 | M | Hypermobility / BJHS | | 0 | | | 6 | | | 1(0) | | | 0 | | | | - | + |
| 655 | *COL3A1* | VUS | | 1 | | | 28 | F | Hypermobility / BJHS | Marfanoid hypermobility syndrome | 1 | | 1 | 7 | 2(2) | | 2(2) | | | 2 | | Normal | | - | - |
| 734 | *COL5A1* | VUS | | 0 | 0 | | 35 | F | Hypermobility / BJHS | | 0 | | | 6 | 3-mild( | 0(0) | 2(0) | | | | 1-a | | | - | + |
| 799 | *COL5A1* | VUS | 0 | 0 | | | 46 | F | Hypermobility / BJHS | | 1 | | | 5 | 1(3) | (3) | 2(0) | | | | | | | | + |
| 801 | | | | | | CNV⌘ *NSD1*:0 *DMPK*: 0 | 9 | F | Hypermobility / BJHS | Hypermobility with significant learning difficulties & epilepsy | 7 | | | 8 | 2(5) | | 1(0) | 2(2) | | | | | | | |
| 814 | *TGFBR2* | Likely Pathogenic $ | | 0 | | | 34 | F | Hypermobility / BJHS | Marfanoid hypermoblity,thin skin, varicose veins,mild blue sclerae | 2 | | | 8 | | 1(1) | 1(3) | 0(2) | | 2 | | | | | + |
| 824 | *COL5A1* | Pathogenic | | | | | | F | Hypermobility / BJHS | | 1 | | | 9 | 1(2) | | 2(3) | | | | | | | | |
| 828 | *COL1A1* | VUS | | 0 | | | 30 | F | Hypermobility / BJHS | Hypermobility, soft skin, easy bruising, tall stature, arterial ectasia, mild varicose veins, early onset of | 3 | | | | 1(4) | | 1(0) | | | 0 | | Normal | (+) | (+) |
| 893 | *COL1A1* | Likely Pathogenic $ | | 0 | | | 51 | F | Hypermobility / BJHS | Hypermobility with pelvic floor weakness, fractured tibia and fibula | 2 | | | | 2(3) | 0(1) | 2(3) | | | 0 | | | | - | - |
| 1151 | *COL1A2* | VUS | | 0 | | | 65 | F | Hypermobility / BJHS | | 2 | | | 4 | 1(2) | 0(1) | 2(0) | | | 0 | | | | + | - |
| 38* | *COL3A1; COL5A2* | VUS; VUS | | 0 | | | 57 | F | Hypermobility / BJHS | Benign connective tissue phenotype with coronary artery dissection | 1 | | | 7 | 3(2) | 1(1) | 2(1) | | | | | Normal | | + | + |
| 39* | *COL1A2; COL3A1* | VUS; VUS | | 0 | 0 | CNV § | 31 | M | Hypermobility / BJHS | Marke hypermobility with bowel fragility | 3(partial) | | 3(TNXB-hets) | | | 1(0) | 1(1) | | | | | | | + | + |
| 57 | | | | | | *PLOD1*: 1 ⬩ | 30 | F | Kyphoscoliosis | | 1 | | 1 | 9 | 3(3) | | 2(2) | 3(4) | | 3 | 1-a | | | | |
| 732 | | | | | | *PLOD1*: 1 ⬩ | 22 | F | Kyphoscoliosis | | 1 | | | 4 | | | 2(0) | 3(3) | | 3 | | | | | |
| 802 | | | | | | *PLOD1*: 1 ⬩ | 10 | F | Kyphoscoliosis | | 2 (partial) | | 2(het) | | 2(1) | 1(0) | 1(1) | 0(4) | | | 1-a | | | | |
| 822 | | | | | | *FKBP14*: 1 *PLOD1*: 0 | 3 | M | Kyphoscoliosis | | 2 | | 2(het) | | | | | 2(1) | | 3 | | | | - | - |
| 36 | *COL1A1* | Pathogenic | 1 | | | | 7 | F | Other HDCT | OI/EDS overlap (pelvic fracture, blue sclerae, hyperextensible skin, hypermobility) | 4 | | | 6 | 0(0) | 0(1) | 2(2) | | | 1 | 2-a,b | | | | |
| 527 | *COL1A1* | Pathogenic | 1 | | | | 28 | F | Other HDCT | Silence type I Osteogenesis Imperfecta/ EDS VIIA or VIIB : repeated fractures, deafness, blue sclerae, kyphosis, early postural hip problems | 2 | | 0/0 | 5 | 0 (1) | 0(0) | 1(0) | | Arthroch alasia type: 1(0) | 3 | 3-a,b,c | Col I | + | + |
| 559 | *COL1A1* | Pathogenic | 1 | | | | 48 | M | Other HDCT | OI/EDS overlap (blue sclera, fractures, slight presenile conductive hearing loss, aortic valve disease, easy bruising, hypermobility, significant family history of vasculopathy) | 5 | | | 4 | 1(3) | 0(3) | | | | 0 | 2-a,b | | | | |
| 629 | *COL1A2* | VUS | 1 | | | | 46 | F | Other HDCT | OI/EDS overlap (mild blue sclerae, fractures, osteopenia, hypermobility, mild skin hyperextensibility), history of recurrent embolism | 7 | | 7/2 | | 0(2) | | 2(0) | | | 2 | 2-a, b | Col I | + | - |
| 804 | *COL1A1* | VUS | | | | *PLOD1*: 0 *TNXB*: 0 | 5 | F | Other HDCT | Congenital hip dysplasia, postural kyphosis, joint hypermobility | 2(partial) | | 0/0 | | 1(3) | 0(0) | 1(2) | 2(2) | | 2 | | | | | |
| 79 | | | | 0 | | *TNXB:1* (VUS), *FBN1*: 0 | 47 | M | Other HDCT with vascular phenotype | Non specific connective tissue phenotype with vascular phenotype (venous aneurysm), generalised hypermobility, skin hyperextensibility, some features of Marfan syndrome, cutis laxa (of the face) and dysmorphic features | 2(mildly) | | | | 2(2) | 0(1) | 2(1) | | | 4 | | Col III | + | + |
| 706 | *TGFBR1* | Likely Pathogenic $ | | 0 | | *TGFBR1:*1 (VUS) | 45 | M | Other HDCT with vascular phenotype | Descending thoracic aortic dissection, subclavian artery aneurysm, pectus excavatum, soft skin | 2 | | | 3 | 1(1) | 1(1) | 1(1) | | | 1 | | | | - | - |
| 708 | *COL3A1* | VUS | | | | | 11 | F | Other HDCT with vascular phenotype | Marfanoid Hypermobility, joint pain, soft thin skin, aortic dilatation, colitis | 5 | | 2 | 4 | 0 | (1) | 1(2) | | | | | | | | |
| 766 | *FBN1* | Pathogenic | | | 0 | | 8 | M | Other HDCT with vascular phenotype | Generalized joint laxity (Hypermobility), marfanoid habitus, mild aortic dilatation, narrow palate, precocious puberty | 0 | | | 7 | 0(0) | 0(0) | 2(0) | 1(1) | Arthroch alasia type: 1(1) | 6 | 1-a | | | | |
| 382 | *SMAD3* | Likely Pathogenic $ | | | | *SMAD3*:1 (VUS) | 49 | F | Other HDCT with vascular phenotype | Hypermobile (9/9), Coronary artery dissection, ASD, Mildly marfanoid features | | | | 9 | 2(2) | 1(0) | 2(3) | | | 2 | | | | | |

EDS, Ehlers-Danlos syndrome. VUS, variant of uncertain clinical significance. Beighton, score for extent of joint hypermobility (/9). OI, osteogenesis imperfecta. HDCT, Hereditary disorder of connective tissue. ASD, atrial septal defect. CNV, copy number variant.

a. Genetic testing by previous Sanger (performed by clinical service, independently of NGS): 1 = alteration identified, 0 =no alteration identified, [blank cells] =not tested
b. Segregation: numbers show the no. affected relatives carrying the variant / no. affected not carrying variant ("affected" =any relative sharing at least one EDS phenotype with index).
c. Ghent systemic score /20
d. Signs of OI: shows the no. and type of signs of OI: a. blue sclera, b. hereditary osteoporosis/fractures, c. presenile conductive hearing loss
e. Biochemical abnormalities: shows collagen type harbouring abnormality by SDS-PAGE

f. LM, Light Microscopy: '+'=abnormal;  '-' = normal; [blank cells]= not tested
g. EM, Electron Microscopy: '+'=abnormal,  '-' = normal,  [blank cells]= not tested,  '++' = collagen rosettes (only in Classical/COL5A1/2 cases)

*IDs 38, 39, 66, 444 had more than one rare variant co-existing. ⌘Karyotyping revealed 0.1 megabase deletion to chromosome q23.1, likely to be a polymorphic CNV (non pathogenic). § TNXB gene duplication  ¶ translocation involving COL3A1 & COL5A2. Not shown: 3 cases of Kyphoscoliotic EDS diagnosed by urinary cross-link assay (PLOD1). Δ Of the 4 affected relatives tested genetically, 1 carried the p.Pro806Leu variant. The 3 who did not carry this variant had joint hypermobility but no other features of EDS.  $ See Table S6 for ACMG classification as Likely Pathogenic.

Supplementary (Appendix, online only material, etc.)

**Table S5** Details of atypical genotype-phenotype correlations identified by the Collagen NGS panel

| Patient ID | Gene | Variant | Variant Classification | Observed phenotype | Functional studies | Family history / Segregation | Comments |
|---|---|---|---|---|---|---|---|
| 636 | *COL3A1* | c.2329G>C: p.G777R | Pathogenic | Classical EDS. Clear phenotype - markedly hyperextensible skin, generalised hypermobility (Beighton 8) including marked distal hypermobility, facies suggestive of Classical EDS, no criteria met for Vascular EDS | Collagen Proteins: normal proα1(III) pattern[a]<br>LM: thickened elastic fibres.<br>EM: irregular packing of collagen fibrils (no collagen rosettes) | Not known | Not detected in clinical setting. |
| 417 | *COL3A1* | c.1922_1923 +2delAAGT | Pathogenic | Classical/Hypermobility/(vascular) overlap. Widened atrophic scars (marked forehead scarring), no skin thinning, tissue fragility, marked generalised hypermobility (Beighton 6), normal facies, history of colonic perforation. | Collagen proteins: absent proa1(III) and collagen III;<br>LM: marked collagen depletion & increased elastin staining;<br>EM: variable collagen fibril size & shape, dilated rER | Mother[d.], arterial rupture; segregation unknown. | - |
| 1088 | *COL5A1* | c.3164T>A: p.L1055X [b] | Pathogenic | Vascular/classical overlap. Thin translucent skin over anterior chest wall, bruising of the shins, with moderate hyperextensibility of the skin, distal hypermobility | [Not done] | Not known | Not detected in clinical setting. |
| 824 | *COL5A1* | c.4564G>T; p.G1522C | Pathogenic | Hypermobility EDS. Extensive joint hypermobility (Beighton 9/9) with recurrent shoulder dislocations, easy bruising; soft non-hyperextensible skin. | [Not done] | Mother –hypermobility<br>Maternal grandfather - sudden cardiac death | Not detected in clinical setting. |
| 893 | *COL1A1* | c.2980C>T: p.R994C [c] | Likely Pathogenic | Hypermobility EDS. Predominant hypermobility trait with hyperextensible skin, marked pelvic floor weakness, history of fractured tibia and fibula. | Collagen proteins: [not done].<br>LM, EM: non-specific | Incomplete segregation of phenotype: Daughter-hypermobile, variant negative; Mother[d.] - hypermobile with pelvic floor weakness, genotype unknown | Not detected in clinical setting. |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 629 | *COL1A2* | c.2123G>A: p.R708E **d** | Uncertain significance | Other HDCT. Juvenile hypermobility, now mild hypermobility, very mildly blue sclera 1/6, osteopenia | Collagen proteins: broadening of Proα2(I) band.<br>LM: moderately increased elastin:collagen ratio.<br>EM: relatively normal | Incomplete segregation: 7 offspring affected with mild connective tissue phenotype; 2/7 carry variant (one had hypermobility with history of fractures, one had hypermobility only) | - |

EDS, Ehlers-Danlos syndrome, VUS, variant of uncertain clinical significance. HGMD, human genetic mutation database. (CM- no's are specific to HGMD entries). LOVD, Leiden Open Variation Database. Beighton, score for extent of hypermobility /9. LM, light miscroscopy. EM, electron microscopy. [d.], deceased Variant classification is as described in the Methods and for those variants not known to be pathogenic, using ACMG criteria (Richards et al. *Genet Med* 2015 [16]), see footnotes c. & d.

**a.** Pepsinised medium not done due to technical reasons. **b.** pathogenic *COL5A1* variant (p.Gly1537Val) causing vascular EDS phenotype also reported in LOVD (Munroe et al.) **c.** Helical R/C variants known to be pathogenic in *COL1A1* (ACMG criteria supporting this variant: 2 Moderate & 4 Supporting criteria); R/C variant also observed in *COL1A2* in Patient ID 1151 - hypermobility EDS with mild phenotype). **d.** Previously reported in a marfanoid hypermobile patient with slow migration of proa2(I) on SDS PAGE (HGMD CM900074; DBSNP rs72658163), this variant classified as “Uncertain significance” owing to contradictory evidence for and against pathogenicity

Supplementary (Appendix, online only material, etc.)

**Table S6** Rare variants identified in Aortopathy-susceptibility genes

| Patient ID | Diagnosis | Clinical details | Gene | Variant | Variant Classification | Novel/reported: Phenotype | Pathogenicity details | Previously detected? |
|---|---|---|---|---|---|---|---|---|
| 66 | Other HDCT (vascular) | Hypermobility / non-Marfan fibrinillopathy (Ghent =1), short stature, ectopia lentis, Aortic & Mitral valve surgery<br>Family history: sudden death (father) & mitral valve prolapse (sister, first cousin) | *FBN1* | c.3781T>A: p.Tyr1261Asn | Pathogenic | Reported: Marfan **a** | Known interacting domain of FBN1, highly conserved residue.<br>In silico predictions: deleterious | Y |
| 378 | Other HDCT (vascular) | Hypermobility, carotid artery dissection, early onset osteoarthritis | *FBN1* | c.1775G>A: p.Gly592Asp | Pathogenic | Reported: Marfan **b** | Known pathogenic | N |
| 766 | Other HDCT (vascular) | Generalized joint laxity (hypermobility), marfanoid habitus, mild aortic dilatation narrow palate, precocious puberty, parental consanguinity | *FBN1* | c.C3373T: p.Arg1125X | Pathogenic | Reported: Marfan **c** | Known pathogenic | N |
| 706 | Other HDCT (vascular) | Descending thoracic aortic dissection, subclavian artery aneurysm, pectus excavatum, soft skin | *TGFBR1* | c.T827C: p.Leu276Pro | Likely Pathogenic **d** | Novel | Ser-Thr kinase domain: multiple mutations in this region observed in LDS/Marfan spectrum - p.267 is closest. Conserved residue,<br>In silico predictions: all deleterious | Y |
| 382 | Other HDCT (vascular) | Hypermobile (9/9), coronary artery dissection, ASD, Mildly marfanoid features (Ghent = 2) | *SMAD3* | c.1218G>C: p.Trp406Cys | Likely Pathogenic **e** | Novel | Proximate to MH2 domain (key interacting domain for other SMADs)<br>In silico predictions: all deleterious | Y |
| 814 | Hypermobile | Marfanoid hypermobility, thin skin, varicose veins, mild blue sclerae. Family history of thoracic aortic rupture(sister), marfanoid features(sister, father) | *TGFBR2* | c.T1538C: p.Val513Ala | Likely Pathogenic **f** | Novel | Ser-Thr kinase domain: multiple mutations in this region observed in LDS/Marfan spectrum - p.C514R is closest. Conserved residue,<br>In silico predictions: mostly deleterious | N |
| 475 | Other HDCT | OI/EDS overlap (multiple fractures, mild blue sclerae, soft skin, hypermobility, systolic murmur) | *TGFBR1* | 214A>G: p.Ile72Leu | Uncertain significance **g** | Reported: BAV | Extracellular (ligand binding) domain – variants in this domain reported in LDS;<br>In silico predictions: equivocal | N |

HDCT, hereditary disroder of connective tissue. Ghent, Ghent systemic score for marfan syndrome.HGMD, human genetic mutation database. LDS, Loeys-Dietz syndrome. Ser-Thr, Serine-threonine kinase (main intracellular signalling mechanism of TGFBR). ASD, atrial septal defect. Variant classification is as described in the Methods and for those variants not known to be pathogenic, using ACMG criteria (Richards et al. *Genet Med* 2015 [16]), see footnotes d-g.
"Previously detected": variants detected (Y) or not detected (N) by previous clinical diagnostic testing (Sanger method). **a.** Y1261C (HGMD CM990591 El-Aleem 1999), Y1261D (HGMD CM547000, Arbustini 2005) **b.** HGMD CM013919 Loeys 2001 **c.** HGMD CM055245, Rommel 2005 **d**. ACMG criteria supporting variant: 2 Moderate + 3 Supporting **e**. 2 Moderate + 2 Supporting **f**. 2 Moderate + 4 Supporting **g.** this variant reported by Bonachea et al. (*BMC Med Genomics* 2014;7:56) as a VUS in a bicuspid aortic valve (BAV) series, incomplete evidence of pathogenicity.

Supplementary (Appendix, online only material, etc.)

**Table S7** Detailed phenotypic and genetic background of cases without identified pathogenic variants or variants of unknown significance (VUS).

| Patient ID | Genetic testing by previous Sanger sequencing *[a]* | | | | Age (yrs) | Sex | Initial clinical diagnosis | Phenotype details | No. relatives affected *[b]* | Affected mut.positive/mut.negative | Beighton score (0-9) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | *COL1A1 / COL1A2* | *COL3A1* | *COL5A1 / COL5A2* | Other genes | | | | | | | |
| 56 | | | 0 | | 32 | M | Classical | Clinically & ultrastructurally classical EDS with aortopathy and mitral valve prolapse | | | |
| 445 | | 0 | 0 | | | F | Classical | Complex connective tissue disorder resembling classical EDS with cerebral aneurysm and family history of aortic and cerebral aneurysm. | | | |
| 595 | | 0 | | | 31 | M | Classical | Clinically classical EDS with family history of young onset cerebrovascular accident in first degree relative. | | | 6 |
| 431 | 0 | | | | 31 | F | Classical/ hypermobility overlap | | 1 | | 7 |
| 534 | | 0 | | | 34 | F | Classical/ hypermobility overlap | Generalised hypermobility with easy bruising, atrophic scars, slow wound healing, increased skin extensibility, | | | 9 |
| 537 | | 0 | | | 30 | F | Classical/ hypermobility overlap | | | | 8 |
| 577 | | | | | 22 | F | Classical/ hypermobility overlap | | | | 8 |
| 717 | | | 0 | | 23 | F | Classical/ hypermobility overlap | Hypermobility with easy bruising, skin hyperextensibility. | | | 7-8 out of 9 |
| 803 | 0 | | | | 28 | F | Classical/ hypermobility overlap | Joint hypermobility and skin hyperextensibility along with oesteopaenia & multiple fractures. Kyphoscoliotic type excluded on preliminary urine cross-link analysis. | | | 8 |
| 1002 | | 0 | | *TNXB: 0* | 53 | F | Classical/ hypermobility overlap | Generalized joint hypermobility with skin involvement and positive family history as well as gastroparesis and gastrointestinal transit problems. | | | 7 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 44 | | | 31 | F | Vascular / Hypermobility overlap | Vascular EDS facies, hypermobile, joint discomfort | 1 | 0 | 5 |
| 73 | | | 12 | M | Vascular | Borderline Vascular / Hypermobility EDS: hypermobility with vascular phenotype and family history of cerebrovascular event | 2 | | 5 |
| 372 | | | 40 | F | Vascular | Atypical case of marked acrogeria and skin fragility | | | |
| 482 | | | 28 | F | Vascular / Hypermobility overlap | Borderline Vascular / Hypermobility EDS: generalised joint hypermobility with skin thinning and tissue fragility; marfanoid skeletal features with complex family history of variable connective tissue disease. | | | 6 |
| 484 | | | 39 | F | Vascular | Mixed connective tissue phenotype with features of vascular and hypermobility EDS and cerebral haemorrhage. | | | 5 |
| 570 | | | 48 | M | Vascular / Hypermobility overlap | Hypermobility EDS phenotype, although there are some facial features reminiscent of Vascular EDS | | | 6 |
| 798 | | | 25 | F | Vascular / Hypermobility overlap | Borderline Vascular / Hypermobility EDS: Clinically, overlap between vascular and hypermobile EDS with cerebral haemorrhage. | | | 5 |
| 50 | 0 | | 37 | F | Hypermobility / BJHS | | 2 | 0 | 5 |
| 61 | | | 35 | F | Hypermobility / BJHS | | | | |
| 64 | | | 12 | F | Hypermobility / BJHS | | 4 | | 5 |
| 65 | | | 60 | F | Hypermobility / BJHS | Sheehan syndrome, femoral rupture in pregnancy. | | | 3 |
| 69 | | *PLOD1: 0* | 14 | F | Hypermobility / BJHS | Hypermobility EDS with accompanying features of kyphoscoliosis. | 2 | | 6 |
| 70 | | | 10 | M | Hypermobility / BJHS | | 2 | | 4 |
| 74 | | | 50 | F | Hypermobility / BJHS | Hypermobility syndrome with family history of aneurysms. | | | |
| 98 | 0 | *PLOD1: 0* | 61 | M | Hypermobility / BJHS | Borderline: Hypermobility EDS with marfanoid featuresand multifocal vascular aneurysm. | | | 8 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 100 | 0 | 0 | | 54 | F | Hypermobility / BJHS | Borderline: Generalized joint hypermobility, skin involvement, cerebral aneurysm. | 2 | 7 |
| 107 | | 0 | *FBN1: 0, ACTA2: 0, MYH11: 0, TGFBR1: 0, TGFBR2: 0* | 47 | M | Hypermobility / BJHS | Borderline:Hypermobility with aortopathy. | | 4 |
| 379 | 0 | 0 | *TNXB: 0* | 58 | F | Hypermobility / BJHS | Marfanoid Hypermobility type with familial recurrent pneumothorax and family history of cerebral aneurysm. | | 0 |
| 381 | | | | 34 | F | Hypermobility / BJHS | | | |
| 389 | | 0 | | 47 | F | Hypermobility / BJHS | Complex of Hypermobile EDS with familial cardiovascular defects / aortopathy and early-onset osteoporosis. | | |
| 406 | | 0 | | 43 | F | Hypermobility / BJHS | Uncomplicated hypermobility EDS with family history of aneurysm. | | 4 |
| 408 | | | *TNXB: 0* | | F | Hypermobility / BJHS | | | 4 |
| 409 | 0 | | | 46 | F | Hypermobility / BJHS | Hypermobility EDS with aortic dilatation | | |
| 428 | | | 0 | 67 | F | Hypermobility / BJHS | Borderline: Overlap between Classical and hypermobility EDS with early onset osteoarthritis and gum recession. | | |
| 495 | | 0 | | 41 | F | Hypermobility / BJHS | Borderline: Hypermobility EDS with significant tissue fragility presenting multiple severe signs of pelvic floor weakness. | | 6 |
| 533 | | | | 34 | F | Hypermobility / BJHS | | | 9 |
| 535 | | | | 4 | M | Hypermobility / BJHS | Hypermobility with upper GI dysmotility. | | |
| 536 | | | | 43 | M | Hypermobility / BJHS | Mild connective tissue phenotype with familial dilated cardiomyopathy and multiple pneumothoraces. | | 1 |
| 576 | | | 0 *FBN1: 0* | 17 | M | Hypermobility / BJHS | Hypermobility with Marfanoid features. | | 9 |
| 578 | | | 0 | 37 | M | Hypermobility / BJHS | Initial diagnosis: Hypermobility EDS / BJHS; later rosettes on EM, suggested possible Classical / Hypermobility overlap. | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 594 | | | | 11 | F | Hypermobility / BJHS | | 7 |
| 621 | | | | 22 | F | Hypermobility / BJHS | | 6 |
| 623 | | | | 54 | F | Hypermobility / BJHS | Hypermobility,family history of sudden cardiac death, mitral valve prolapse. | |
| 630 | | | | 36 | F | Hypermobility / BJHS | | 7 |
| 631 | | | | 51 | F | Hypermobility / BJHS | | 8 |
| 635 | | | | 41 | F | Hypermobility / BJHS | | 7 |
| 639 | | | | 38 | F | Hypermobility / BJHS | Hypermobility EDS with marfanoid habitus. | 5 |
| 649 | | | | 26 | M | Hypermobility / BJHS | | 3 |
| 650 | 0 | | | 36 | F | Hypermobility / BJHS | | 7 |
| 669 | 0 | | | 29 | F | Hypermobility / BJHS | | 7 |
| 670 | | | | 36 | F | Hypermobility / BJHS | Extreme generalised hypermobility with pelvic floor weakness. | 8 |
| 673 | 0 | 0 | | 57 | M | Hypermobility / BJHS | Hypermobility with marfanoid features. | 3 |
| 676 | | 0 | | 35 | F | Hypermobility / BJHS | | 5 |
| 681 | | | | 53 | F | Hypermobility / BJHS | Hypermobility and congenital kyphoscoliosis. | |
| 761 | | | *PLOD1: 0* | 22 | M | Hypermobility / BJHS | Borderline: Hypermobility with marfanoid features. | 6 |
| 764 | | 0 | *COL9A3: 0* | 10 | M | Hypermobility / BJHS | Borderline – other: Extreme connective tissue phenotype – overlap between classical and kyphoscoliotic type EDS. | 9 |
| 767 | | | | 54 | F | Hypermobility / BJHS | Hypermobility with mitral valve prolapse and family history of cerebral anuerysm. | 5 |
| 769 | | | | 22 | F | Hypermobility / BJHS | Borderline: Hypermobility with recurrent fracture, brachydactylys and dysautonomia | 3 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 778 | | | | 22 | F | Hypermobility / BJHS | Hypermobility with family history of cerebrovascular accident. | 7 |
| 781 | | | | 40 | F | Hypermobility / BJHS | Hypermobility with intracranial haemorrhage and bleeding tendency. | 5 |
| 806 | | | | 16 | M | Hypermobility / BJHS | | |
| 821 | | | | 3 | M | Hypermobility / BJHS | | 8 |
| 825 | | | 0 *PLOD1: 0, TNXB: 0* | 3 | F | Hypermobility / BJHS | Unusual form of Hypermobility EDS III with features overlapping with other subtypes and probably compound heterozygote inheritance. | |
| 826 | | | | 17 | F | Hypermobility / BJHS | | 7 |
| 827 | 0 | | | 29 | M | Hypermobility / BJHS | Hypermobility EDS with marfanoid habitus. | 6 |
| 829 | | | 0 | 2 | M | Hypermobility / BJHS | Mild connective tissue phenotype with some extensive pretibial bruising and ultrastructural evidence of collagen disruption (?classical EDS) | 0 |
| 872 | | | *FBN1: 0* | 5 | F | Hypermobility / BJHS | | 8 |
| 888 | | 0 | | 16 | F | Hypermobility / BJHS | | 5 |
| 891 | | | | 33 | F | Hypermobility / BJHS | Familial Hypermobiliity with unusual feature of skin thinning and variable marfanoid features co-segregating. | 4 |
| 922 | | 0 | | 37 | F | Hypermobility / BJHS | | 6 |
| 1083 | | | | 4 | F | Hypermobility / BJHS | | 9 |
| 1085 | | | | 31 | F | Hypermobility / BJHS | | 3 |
| 1089 | | | | 22 | F | Hypermobility / BJHS | Hypermobility with family history of marfanoid habitus and aortic aneurysm. | 4 |
| 1108 | | | | 44 | F | Hypermobility / BJHS | | 7 |
| 1297 | | | | 15 | M | Hypermobility / BJHS | Soft stretchy skin and joint hypermobility along with multiple exostoses and vertebral artery dissection. | 4 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1338 | | | | 13 | F | Hypermobility / BJHS | Hypermobility with kyphosis. | | | 8 |
| 88 | | 0 | *COL3A1: 0* | 12 | F | Complex EDS | Borderline (other):Connective tissue phenotype with features of Vascular and Periodontitis EDS. | | | 7 |
| 357 | | 0 | | 12 | M | Complex EDS | Vascular and Periodontitis EDS: acrogeria, easy bruising, marked generalised periodontal recession. | | | |
| 682 | | 0 | | 45 | F | Complex EDS | indeterminate: Early periodontal disease / BJHS. | | | 6 |
| 718 | 0 | | 0 | 32 | F | Complex EDS | Indeterminate: Complex EDS phenotype overlap of Classical / Vascular / Hypermobility EDS. | | | 5 |
| 820 | | | 0 | 3 | F | Complex EDS | Borderline other: Mostly Arthrochalasia EDS, but with some features of Kyphoscoliosis EDS and minor features of Classicall EDS | | | |
| 823 | | | | 6 | M | Complex EDS | Borderline other: Very hypermobile with features of number of different overlapping EDS subtypes. | | | 8 |
| 890 | | 0 | | 55 | F | Complex EDS | Indeterminate: a rare Ehlers-Danlos Syndrome subtype. | | | 4 |
| 1092 | | 0 | | 20 | F | Complex EDS | Borderline other: skin bruisability, skin thinning. | | | |
| 1109 | | | 0 *TNXB: 0* | 54 | F | Complex EDS | Borderline other: bilateral congenitally dislocated hips, scoliosis and pelvic tilt. | | | |
| 812 | 0 | 0 | *PLOD1: 0 ,FKBP14: 0, CHST14: 0* | 2 | F | Kyphoscoliotic EDS | | | | |
| 1283 | | | | 31 | M | Kyphoscoliotic EDS | Type VI: severe EDS combination of early onset scoliosis operated upon at the age of 8, osteotomies of his hip, stabilisation of one of his knees | 1 | 0 | |
| 810 | | | | 15 | M | Complex EDS | Indeterminate: Complex phenotype including overlap between marfanoid Hypermobility, Classical and Kyphoscoliotic EDS. | | | 8 |
| 479 | 0 | | | 24 | F | Other HDCT | Indeterminate: possibility of chromosomal imbalance, Stickler syndrome, a possibility of neuromuscular disorder. | | | 9 |
| 568 | | | | 4 | F | Other HDCT | Indeterminate, Urinary cross link normal. | | | |
| 620 | | | *PLOD1: 0* | 21 | F | Other HDCT | indeterminate: Ehlers-Danlos Syndrome/myopathy overlap, urinary cross link normal. | | | 5 |
| 628 | | | | 49 | F | Other HDCT | Indeterminate: borderline between an EDS variant and an acquired cutis laxa. | | | 5 |
| 654 | | | | 47 | F | Other HDCT | Indeterminate | | | 5 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 45 | 0 | 0 | | | 52 | f | Other HDCT(vascular) | Indeterminate: hypermobility with carotid dissection. | | | |
| 16 | | | 0 | | 51 | m | Other HDCT (vascular) | Other HDCT: hypermobility with aortopathy and family history of aortic aneurysm. | 2 | | 4 |
| 33 | | 0 | | | 45 | f | Other HDCT (vascular) | Features of Marfan and EDS and coronary artery dissection and family history of vascular disease. | 1 | 0 | 9 |
| 35 | 0 | 0 | | | 32 | f | Other HDCT (vascular) | Indeterminate: Joint hypermobility, atrophic scars, carotid dissection. | 2 | 0 | |
| 40 | 0 | 0 | | *TGFB1: 0, TGFB2: 0* | 54 | M | Other HDCT (vascular) | Indeterminate: multiple aneurysms, slightly soft skin. | 3 | 0 | |
| 60 | | 0 | | | 48 | M | Other HDCT (vascular) | Indeterminate: soft extensible skin, striae, bilateral carotid dissection. | 1 | | |
| 72 | | 0 | 0 | | 53 | M | Other HDCT (vascular) | Indeterminate: Joint hypermobility, skin hyperextensibility, carotid dissection and family history of aortic aneurysms. | | | |
| 99 | | 0 | | | 60 | M | Other HDCT (vascular) | Indeterminate: non-specific connective tissue features with carotid dissection. | | | 0 |
| 385 | | 0 | | | 34 | F | Other HDCT (vascular) | Hypermobility with mitral valve prolapse and family history of cerebral and aortic aneurysm. | | | |
| 403 | | 0 | | | 41 | F | Other HDCT (vascular) | Hypermobility with carotid dissection. | | | |
| 421 | | | | | 9 | F | Other HDCT (vascular) | Indeterminate: Complex multisystem familial connective tissue phenotype, including generalised hypermobility, camptodactyly, skin fragility and aortopathy. | 3 | | 8 |
| 425 | | 0 | | | 51 | F | Other HDCT (vascular) | Unspecified: Mild connective tissue phenotype, aortic dilatation, family history of hypermobility. | | | 3 |
| 446 | | 0 | | | 49 | M | Other HDCT (vascular) | Unspecified: Non-specific mild connective tissue phenotype with vascular event. | | | 4 |
| 453 | | 0 | | | 48 | F | Other HDCT (vascular) | Indeterminate: Non specific, mild connective tissue phenotype with hypermobility, carotid dissection. | | | 4 |
| 474 | 0 | 0 | | | 63 | F | Other HDCT (vascular) | Indeterminate: Non-specific connective tissue phenotype with thin skin, easy bruising, spontaneous epidural haemorrhage. | | | 0 |
| 532 | | 0 | | | 41 | M | Other HDCT (vascular) | Indeterminate: Mild connective tissue phenotype with aortopathy and polydactyly and hip dysplasia. | | | 2 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 564 | 0 | 0 | 0 | *FBN1: 0, TGFBR1: 0, TGFBR2: 0* | 24 | M | Other HDCT (vascular) | EDS hypermobility/OI overlap: EDS hypermobility with aortic dilatation some similarities to classical EDS, a compound heterozygosity of his father's HOCM genes with his mother's hypermobile one, urinary test normal. | 8 |
| 567 | | 0 | | | 53 | M | Other HDCT (vascular) | Indeterminate HDCT: mild hypermobility and connective tissue phenotype with iliofemoral arterial aneurysms. | 4 |
| 651 | | 0 | | *GLUT10: 0, TGFBR1: 0, TGFBR2: 0, FBLN4: 0, SLC2A10: 0* | 27 | F | Other HDCT (vascular) | Familial Marfanoid hypermobility syndrome with family history of carotid and cerebral aneurysm and early onset varicose veins. | |
| 768 | | 0 | | | 54 | M | Other HDCT (vascular) | Indeterminate: Mild connective tissue symptoms with marfanoid habitus and multifocal vascular disease. | 3 |
| 777 | | 0 | | | 29 | F | Other HDCT (vascular) | Indeterminate: Hypermobility with early onset osteoarthritis and family history of cerebral aneurysm. | 7 |
| 800 | | 0 | | | 60 | F | Other HDCT (vascular) | Indeterminate: Non-specific hereditary disorder of connective tissue with multiple vascular haemorrhages and inflammatory arthropathy. | |
| 964 | | | | | 72 | F | Other HDCT (vascular) | Other HDCT: Hypermobility with familial cerebral aneurysm/aortic aneurysm in multiple siblings. | 7 |
| 1093 | | | | | 47 | F | Other HDCT (vascular) | Coronary artery dissection | |
| 1185 | | 0 | | | 43 | F | Other HDCT (vascular) | Hypermobility with an unexpected aneurysm. | |

EDS, Ehlers-Danlos syndrome. VUS, variant of uncertain clinical significance. Beighton, score for extent of joint hypermobility (/9). OI, osteogenesis imperfecta. HDCT, Hereditary dis

a. Genetic testing by previous Sanger (performed by clinical service, independently of NGS): 1 = alteration identified, 0 =no alteration identified, [blank cells] =not tested

b. Segregation: numbers show the no.affected relatives carrying the variant / no. affected not carrying variant ("affected" =any relative sharing at least one EDS phenotype with index)

c. Ghent systemic score /20

d. Signs of OI: shows the no. and type of signs of OI: a. blue sclera, b. hereditary osteoporosis/fractures, c. presenile conductive hearing loss

e. Biochemical abnormalities: shows collagen type harbouring abnormality by SDS-PAGE

f. LM, Light Microscopy: '+'=abnormal; '-' = normal; [blank cells]= not tested

g. EM, Electron Microscopy: '+'=abnormal, '-' = normal, [blank cells]= not tested, '++' = collagen rosettes (only in Classical/COL5A1/2 cases)

| Villefranche criteria - No.major criteria(No. of minor criteria) | | | | | Ghent *[c]* | Signs OI *[d]* | Biochem *[e]* | LM *[f]* | EM *[g]* |
|---|---|---|---|---|---|---|---|---|---|
| Classical | Vascular | Hypermob | Kyphoscol | Other EDS | | | | | |
| 3(4) | 0(0) | 2(2) | 0(0) | 0(0) | 3 | | | + | + |
| 3(5) | 0(0) | 0 | 0(0) | 0(0) | 1 | | Col III | + | + |
| 2(3) | 0(0) | 2(0) | 0(0) | 0(0) | 3 | | | | − |
| 1(4) | 0(0) | 2(3) | 0(0) | 0(0) | | | | − | − |
| 3(2) | 1(2) | 2(2) | 0(0) | 0(0) | | | Col III | + | − |
| 2(1) | 0(0) | 2(1) | 0(0) | 0(0) | | 1-a | normal | − | + |
| 2(2) | 0(0) | 2(1) | 0(0) | 0(0) | | 1-a | | + | + |
| 1(2) | 0(0) | 2(1) | 0(0) | 0(0) | | | | | + |
| 2(3) | 0(0) | 2(3) | 0(0) | 0(0) | | 1-a | Normal | | |
| 2(2) | 0(0) | 2(2) | 0(0) | 0(0) | | | Normal | | − |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 0(0) | 1(1) | 2(2) | 0(0) | 0(0) | 0 | | | − | − |
| 0(0) | 2(2) | 2(1) | 0(0) | 0(0) | | | | | |
| 0(0) | 2(4) | 0(0) | 0(0) | 0(0) | | | | + | + |
| 0(0) | 1(1) | 2(2) | 0(0) | 0(0) | 2 | | Normal | | − |
| 0(0) | 2(4) | 1(0) | 0(0) | 0(0) | 2 | 1-a | Normal | | + |
| 0(0) | 1(2) | 2(1) | 0(0) | 0(0) | 2 | 1-a | Normal | + | + |
| 0(0) | 3(1) | 2(1) | 0(0) | 0(0) | | | | | |
| 2(1) | 1(0) | 1(2) | 0(0) | 0(0) | | | | | − |
| 0(0) | 0(0) | 2(0) | 0(0) | 0(0) | | | | | + |
| 0(1) | 0(0) | 2(2) | 0(0) | 0(0) | | | | | − |
| 0(0) | 2(0) | 1(0) | 0(0) | 0(0) | | | | | |
| 0(0) | 0(0) | 2(2) | 2(0) | 0(0) | | | | | − |
| 0(1) | 0(0) | 1(1) | 0(0) | 0(0) | | | | | |
| 1(0) | 0(2) | 1(1) | 0(0) | 0(0) | | | | | + |
| 0(0) | 1(1) | 2(1) | 0(0) | 0(0) | 3 | | | | − |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 2(1) | 1(0) | 2(1) | 0(0) | 0(0) | | | | + |
| 0(0) | 1(1) | 2(1) | 0(0) | 0(0) | | | | + |
| 0(1) | 0(0) | 2(2) | 0(0) | 0(0) | 5 | | | |
| 1(0) | 0(0) | 1(2) | 0(0) | 0(0) | | | | |
| 0(3) | 0(0) | 2(3) | 0(0) | 0(0) | | | | − |
| 0(0) | 1(1) | 1(1) | 0(0) | 0(0) | | | | |
| 2(1) | 0(0) | 2(1) | 0(0) | 0(0) | | | | − |
| 0(0) | 0(0) | 2(3) | 0(0) | 0(0) | | 1-a | | |
| 2(3) | 0(0) | 2(1) | 0(0) | Periodontitis (1 criterion) | | | | |
| 1(3) | 0(0) | 1(3) | 0(0) | 0(0) | 2 | | | − |
| 1(2) | 0(0) | 2(2) | 0(0) | 0(0) | | | | − |
| 0(0) | 0(0) | 1(1) | 0(0) | 0(0) | | | | |
| 0(0) | 0(0) | 1(0) | 0(0) | 0(0) | 5 | 1-a | | + |
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | 7 | | | + |
| 0(0) | 0(0) | 0(0) | 0(0) | 0(0) | | | | + |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 1(2) | 0(0) | 1(1) | 0(0) | 0(0) | | | | | |
| 0(0) | 0(0) | 2(2) | 0(0) | 0(0) | | | 1-a | | |
| 0(1) | 0(0) | 1(1) | 0(0) | 0(0) | | | 1-a | − | |
| 1(2) | 0(0) | 2(2) | 0(0) | 0(0) | | | | − | − |
| 0(0) | 0(0) | 1(1) | 0(0) | 0(0) | | | | + | − |
| 0(0) | 0(0) | 1(1) | 0(0) | 0(0) | | | | + | − |
| 0(0) | 0(0) | 2(2) | 0(0) | 0(0) | | 3 | 1-a | − | − |
| 0(0) | 0(0) | 1(0) | 0(0) | 0(0) | | | | | − |
| 0(0) | 0(0) | 1(0) | 0(0) | 0(0) | | | | − | − |
| 1(2) | 0(0) | 2(1) | 0(0) | 0(0) | | | 1-a | − | − |
| 0(0) | 0(0) | 2(2) | 0(0) | 0(0) | | | | − | − |
| 0(1) | 0(0) | 1(1) | 0(0) | 0(0) | | 3 | a | + | − |
| 0(0) | 0(0) | 2(2) | 0(0) | 0(0) | | | | | + |
| 0(0) | 0(0) | 1(3) | 1(0) | 0(0) | | 1 | | − | − |
| 1(2) | 0(0) | 2(1) | 3(3) | 0(0) | | 3 | | | |
| 2(4) | 0(0) | 2(1) | 3(2) | 0(0) | | 2 | | | + |
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | | 1 | | − | − |
| 0(0) | 0(0) | 1(3) | 0(0) | 0(0) | | | | | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 0(0) | 0(0) | 2(3) | 0(0) | 0(0) | | | | − | − |
| 2(0) | 1(0) | 2(2) | 0(0) | 0(0) | | | | − | − |
| 0(0) | 0(0) | 1(1) | 1(1) | 0(0) | | | | − | − |
| 0(0) | 0(0) | 2(2) | 2(1) | 0(0) | | | | − | − |
| 1(4) | 0(0) | 2(2) | 2(0) | 0(0) | | | 1-a | | + |
| 0(0) | 0(0) | 2(0) | 0(0) | 0(0) | | | 1-a | | |
| 0(0) | 0(0) | 1(1) | 0(0) | 0(0) | | 2 | | | |
| 0(2) | 0(0) | 1(1) | 0(0) | 0(0) | | | | + | + |
| 0(0) | 0(0) | 1(2) | 0(0) | 0(0) | | | | | |
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | | | | | |
| 0(0) | 1(0) | 1(3) | 0(0) | 0(0) | | 2 | | | |
| 1(1) | 0(0) | 2(1) | 0(0) | 0(0) | | | 1-a | − | − |
| 0(0) | 0(0) | 1(3) | 0(0) | Arthrochalasia - 2(0) | | | 1-a | | |
| 0(0) | 0(0) | 1(2) | 0(0) | 0(0) | | | | − | + |
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | | 1 | 1-a | | |
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | | | | | |
| 0(0) | 1(0) | 1(1) | 0(0) | 0(0) | | | | | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 0(0) | 0(0) | 2(1) | 0(0) | 0(0) | | 1-a | | | |
| 0(0) | 3(2) | 1(0) | 0(0) | Periodontitis - 1(0) | | | Col III | | |
| 0(0) | 2(2) | 0(0) | 0(0) | Periodontitis - 1(0) | | 1-a | | + | + |
| 0(0) | 0(0) | 1(2) | 0(0) | 0(0) | | 1-a | | + | − |
| 2(2) | 3(1) | 2(1) | 0(0) | 0(0) | | 1-a | | + | + |
| 1(1) | 0(0) | 0(0) | 1(0) | Arthrochalasia - 2(2) | | | | + | + |
| 1(5) | 2(0) | 2(2) | 2(2) | 0(0) | 2 | | | − | − |
| 0(0) | 0(0) | 0(1) | 0(0) | 0(0) | | | | | |
| 2(1) | 0(0) | 0(0) | 0(0) | 0(0) | | | | | |
| 2(1) | 0(0) | 0(0) | 0(0) | Arthrochalasia - 0(1) | | | | | |
| 0(0) | 0(0) | 1(1) | 3(2) | 0(0) | 2 | | | | − |
| 0(0) | 0(0) | 0(0) | 2(1) | 0(0) | | | | | |
| 2(4) | 0(0) | 2(2) | 2(2) | 0(0) | 2 | | − | | |
| 1(3) | 1(0) | 2(0) | 2(1) | 0(0) | | | Col I | − | − |
| 0(2) | 0(0) | 0(0) | 1(0) | 0(0) | | | | | + |
| 1(2) | 0(0) | 1(3) | 2(2) | 0(0) | | | | | |
| 2(2) | 0(0) | 2(1) | 0(0) | 0(0) | | | | + | |
| 0(0) | 0(0) | 1(1) | 0(0) | 0(0) | | | | | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 1(0) | 1(0) | 1(1) | 0(0) | 0(0) | | | Normal | + | + |
| 2(1) | 0(1) | 1(3) | 0(0) | 0(0) | 0 | | Normal | − | + |
| 0(0) | 1(0) | 1(1) | 0(0) | 0(0) | 8 | | | − | − |
| 0(1) | 3(1) | 0(0) | 0(0) | 0(0) | | | Col III | − | − |
| 0(1) | 1(0) | 2(1) | 0(0) | 0(0) | 1 | | Col III | + | + |
| 1(0) | 1(0) | 0(0) | 0(0) | 0(0) | | | | + | − |
| 0(0) | 1(1) | 0(0) | 0(0) | 0(0) | | | | − | + |
| 0(1) | 1(1) | 0(0) | 0(0) | 0(0) | | | | | |
| 0(0) | 0(0) | 2(2) | 0(0) | 0(0) | 2 | | | − | − |
| 0(0) | 1(0) | 1(0) | 0(0) | 0(0) | | | | + | + |
| 2(6) | 1(3) | 2(3) | 0(0) | 0(0) | 2 | | | | |
| 2(0) | 0(0) | 2(1) | 0(0) | 0(0) | | 1-a | | | |
| 0(1) | 1(1) | 1(0) | 0(0) | 0(0) | | | Normal | | + |
| 0(0) | 1(1) | 0(0) | 0(0) | 0(0) | | | Normal | | + |
| 0(1) | 0(1) | 0(0) | 0(0) | 0(0) | | | Normal | + | + |
| 0(0) | 1(0) | 0(0) | 0(0) | 0(0) | 2 | | | − | − |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 2(3) | 0(1) | 2(1) | 0(0) | 0(0) | 4 | 1-a | | + | + |
| 1(0) | 1(0) | 1(0) | 0(0) | 0(0) | 1 | | Normal | + | − |
| 0(0) | 0(2) | 0(1) | 0(0) | 0(0) | 2 | | | | |
| 0(0) | 1(0) | 0(0) | 0(0) | 0(0) | 2 | | | − | − |
| 0(0) | 0(0) | 2(3) | 0(0) | 0(0) | 1 | | | | |
| 0(0) | 1(1) | 1(0) | 0(0) | 0(0) | | | | − | |
| 1(0) | 0(1) | 2(1) | 0(0) | 0(0) | 2 | 1-a | Normal | − | − |
| 0(0) | 1(0) | 0(0) | 0(0) | 0(0) | | | | | |
| 0(0) | 0(0) | 1(0) | 0(0) | 0(0) | | | | | |

sorder of connective tissue. ASD, atrial septal defect. CNV, copy number variant.

). c. Ghent systemic score /20

Supplementary (Appendix, online only material, etc.)

**Table S8** In silico predictions of missense pathogenic variants and variants of uncertain significance

| Patient ID | Gene | Variant | Classification | Coordinates | Max. Freq. | SIFT | | Polyphen | | MutationTaster | | MutationAssessor | | LRT | | FATHMM | | CADD | GERP++ | PhyloP | SiPhy |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | score | prediction | score | prediction | score | prediction | score | prediction | score | prediction | score | prediction | | | | |
| 636 | *COL3A1* | c.2329G>C: p.G777R | pathogenic | 2:189866168 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.87 | H | 1.00 | D | 0.61 | D | 4.003,20.5 | 5.38 | 2.69 | 19.49 |
| 824 | *COL5A1* | c.4564G>T: p.G1522C | pathogenic | 9:137713952 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.82 | H | 1.00 | U | 0.63 | D | 3.577,18.22 | 4.70 | 2.14 | 17.22 |
| 62 | *COL5A2* | c.3445G>T: p.G1149C | pathogenic | 2:189907903 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.90 | H | 1.00 | D | 0.62 | D | 4.220,21.9 | 5.39 | 2.68 | 19.52 |
| 36 | *COL1A1* | c.643G>A:p.G215S | pathogenic | 17:48275146 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.84 | H | 1.00 | D | 0.63 | D | 4.445,23.7 | 4.80 | 2.36 | 17.02 |
| 559 | *COL1A1* | c.662G>C: p.G221A | pathogenic | 17:48275127 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.87 | H | 1.00 | D | 0.63 | D | 3.700,18.79 | 4.80 | 2.36 | 17.02 |
| 37 | *COL3A1* | c.2564G>A: p.G855D | pathogenic | 2:189868147 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.80 | H | 1.00 | D | 0.59 | D | 4.275,22.3 | 5.61 | 2.65 | 19.65 |
| 42 | *COL3A1* | c.2417C>T: p.P806L | pathogenic | 2:189867049 | NA | 0.96 | D | 0.06 | B | 1.00 | D | 0.62 | L | 1.00 | D | 0.54 | D | 3.877,19.70 | 5.77 | 2.73 | 19.99 |
| 46 | *COL3A1* | c.G1771: p.G591R | pathogenic | 2:189861900 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.82 | H | 1.00 | D | 0.63 | D | 4.290,22.4 | 6.03 | 2.87 | 20.16 |
| 76 | *COL3A1* | c.2771G>A: p.G924D | pathogenic | 2:189868817 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.84 | H | 1.00 | D | 0.63 | D | 5.324,34 | 5.50 | 2.59 | 19.41 |
| 733 | *COL3A1* | c.2816G>A: p.G939D | pathogenic | 2:189868862 | NA | 1.00 | D | 0.98 | D | 1.00 | D | 0.87 | H | 1.00 | D | 0.63 | D | 3.773,19.16 | 5.63 | 2.66 | 19.69 |
| 448 | *COL3A1* | c.4319C>T: p.P1440L | pathogenic | 2:189876418 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.78 | M | 1.00 | D | 0.49 | D | 4.798,27.1 | 5.70 | 2.69 | 19.83 |
| 66 | *FBN1* | c.3781T>A: p.Y1261N | pathogenic | 15:48776072 | NA | 1.00 | D | 0.99 | D | 1.00 | D | 0.85 | H | 1.00 | D | 0.53 | D | 5.006,29.4 | 6.17 | 2.37 | 16.48 |
| 378 | *FBN1* | c.1775G>A: p.G592D | pathogenic | 15:48800841 | NA | 0.99 | D | 1.00 | D | 1.00 | D | 0.74 | M | 1.00 | D | 0.43 | T | 5.285,33.0 | 5.71 | 2.85 | 18.78 |
| 893 | *COL1A1* | c.C2980T: p.R994C | Likely Pathogenic | 17:48266329 | NA | 1.00 | D | 0.99 | D | 1.00 | D | 0.79 | H | 1.00 | D | 0.49 | D | 3.479,17.80 | 3.83 | 2.00 | 14.74 |
| 814 | *TGFBR2* | c.T1538C: p.V513A | Likely Pathogenic | 3:30732925 | NA | 0.99 | D | 0.70 | P | 1.00 | D | 0.54 | N | 1.00 | N | 0.40 | T | 4.401,23.3 | 4.73 | 1.03 | 13.21 |
| 382 | *SMAD3* | c.1218G>C: p.W406C | Likely Pathogenic | 15:67482814 | NA | 0.97 | D | 1.00 | D | 1.00 | D | 0.73 | M | 1.00 | D | 0.56 | D | 4.218,21.9 | 4.97 | 2.32 | 18.25 |
| 706 | *TGFBR1* | c.T827C: p.L276P | Likely Pathogenic | 9:101904839 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.73 | M | 1.00 | D | 0.41 | T | 4.565,24.7 | 5.87 | 2.37 | 15.56 |
| 49 | *COL3A1* | G3511A: p.G1171K | VUS | 2:189872854 | NA | 0.52 | T | 0.81 | P | 0.70 | D | 0.61 | L | 1.00 | D | 0.52 | D | 4.469,23.9 | 5.51 | 2.59 | 19.42 |
| 478 | *COL1A1* | c.4315A>G: p.I1439V | VUS | 17:48262943 | NA | 0.92 | T | 0.34 | B | 1.00 | D | 0.67 | M | 1.00 | D | 0.44 | T | 1.873,12.22 | 4.49 | 1.89 | 12.90 |
| 828 | *COL1A1* | c.3301G>A: p.E1101K | VUS | 17:48265305 | NA | 0.91 | T | 1.00 | D | 1.00 | D | 0.61 | L | 1.00 | D | 0.52 | D | 5.449,35.0 | 5.00 | 2.32 | 17.08 |
| 39 | *COL1A2* | c.2861T>C: p.I954T | VUS | 7:94055087 | NA | 0.46 | T | 0.00 | B | 0.00 | N | 0.44 | N | 0.72 | N | 0.52 | D | 0.057,4.310 | -0.42 | -0.43 | 5.62 |
| 558 | *COL1A2* | c.1159G>C: p.A387P | VUS | 7:94039801 | NA | | | | | | | | | | | | | 0.023,4.135 | | | |
| 1151 | *COL1A2* | c.C4012T: p.R1338C | VUS | 7:94059616 | NA | 1.00 | D | 1.00 | D | 1.00 | D | 0.74 | M | 1.00 | D | 0.44 | T | 3.598,18.32 | 5.35 | 2.89 | 19.95 |
| 38 | *COL3A1* | c.198A>G: p.I66M | VUS | 2:189849604 | 0.00010 | 0.86 | T | 0.05 | B | 1.00 | D | 0.59 | L | 1.00 | N | 0.42 | T | 3.973,20.3 | -4.78 | -0.55 | 14.85 |
| 39 | *COL3A1* | c.2044G>A: p.E682K | VUS | 2:189864032 | NA | 0.87 | T | 1.00 | D | 1.00 | D | 0.66 | M | 1.00 | D | 0.52 | D | 4.152,21.5 | 4.96 | 2.47 | 18.61 |
| 655 | *COL3A1* | c.3938A>G: p.K1313R | VUS | 2:189875018 | 0.00260 | 0.95 | D | 1.00 | D | 0.86 | D | 0.58 | L | 1.00 | D | 0.43 | T | 3.731,18.95 | 5.93 | 2.26 | 16.38 |
| 66 | *COL5A1* | c.G805A: p.E269K | VUS | 9:137620534 | NA | 0.08 | T | 0.02 | B | 0.95 | D | 0.64 | L | 0.99 | U | 0.49 | D | 1.159,9.720 | 3.93 | 1.72 | 15.92 |
| 734 | *COL5A1* | c.3257C>T: p.A1086V | VUS | 9:137697059 | NA | 0.39 | T | 0.99 | D | 1.00 | D | 0.48 | N | 1.00 | U | 0.52 | D | 2.645,14.80 | 5.19 | 2.41 | 18.70 |
| 799 | *COL5A1* | c.2497C>T: p.P833S | VUS | 9:137676847 | 0.00020 | 0.43 | T | 0.73 | P | 0.74 | D | 0.63 | L | 1.00 | U | 0.55 | D | 1.614,11.35 | 4.39 | 2.00 | 15.75 |
| 38 | *COL5A2* | c.2228A>C: p.K743T | VUS | 2:189923156 | 0.00010 | | | 0.99 | D | 1.00 | D | 0.60 | L | 1.00 | D | 0.52 | D | 2.582,14.60 | 5.56 | 2.24 | 16.02 |
| 671 | *COL5A2* | c.470C>T: p.P157L | VUS | 2:189957133 | 0.00010 | | | 1.00 | D | 1.00 | D | 0.65 | M | 1.00 | D | 0.54 | D | 4.745,26.5 | 5.98 | 2.84 | 17.38 |
| 804 | *COL1A1* | c.584C>T: p.A195V | VUS | 17:48275526 | NA | 0.90 | T | 0.08 | B | 0.76 | D | 0.59 | L | 0.72 | N | 0.53 | D | 4.187,21.7 | 4.10 | 2.55 | 14.50 |
| 629 | *COL1A2* | c.2123G>A: p.R708Q | VUS | 7:94049588 | 0.00080 | 0.99 | D | 0.99 | D | 1.00 | D | 0.57 | L | 1.00 | D | 0.54 | D | 4.603,25.1 | 5.84 | 2.94 | 20.53 |
| 708 | *COL3A1* | c.C2002A: p.P668T | VUS | 2:189863424 | NA | 0.84 | T | 0.85 | P | 1.00 | D | 0.65 | M | 1.00 | D | 0.55 | D | 3.110,16.39 | 5.93 | 2.81 | 19.95 |
| 444 | *COL1A1* | c.G3755A: p.R1252H | VUS | 17:48264060 | 0.00010 | 1.00 | D | 0.62 | P | 0.99 | D | 0.74 | M | 1.00 | D | 0.43 | T | 3.060,16.21 | 4.03 | 2.06 | 15.09 |
| 384 | *COL1A1* | c.3466A>G: p.N1156D | VUS | 17:48264441 | NA | 0.67 | T | 0.54 | P | 1.00 | D | 0.44 | N | 1.00 | D | 0.50 | D | 2.782,15.27 | 3.70 | 1.67 | 11.78 |
| 475 | *TGFBR1* | 214A>G: p.I72L | VUS | 9:101891253 | 0.00030 | 0.16 | T | 0.67 | P | 1.00 | D | 0.53 | N | 1.00 | D | 0.56 | D | 2.997,16.00 | 6.08 | 2.33 | 15.63 |
| **All Pathogenic** | **mean** | | | | | **1.00** | | **0.92** | | **1.00** | | **0.81** | | **1.00** | | **0.59** | | **4.35+** | **5.48** | **2.59** | **18.79** |
| | **s.d.** | | | | | **0.01** | | **0.26** | | **0.00** | | **0.07** | | **0.00** | | **0.07** | | **0.59+** | **0.46** | **0.22** | **1.34** |
| **All Likely Pathogenic** | **mean** | | | | | **0.99** | | **0.92** | | **1.00** | | **0.70** | | **1.00** | | **0.46** | | **4.17+** | **4.85** | **1.93** | **15.44** |
| | **s.d.** | | | | | **0.01** | | **0.15** | | **0.00** | | **0.11** | | **0.00** | | **0.07** | | **0.48+** | **0.84** | **0.62** | **2.11** |
| **All VUS** | **mean** | | | | | **0.70** | | **0.67** | | **0.89** | | **0.60** | | **0.97** | | **0.50** | | **3.04+** | **4.25** | **2.05** | **16.11** |
| | **s.d.** | | | | | **0.30** | | **0.38** | | **0.24** | | **0.08** | | **0.09** | | **0.05** | | **1.50+** | **2.63** | **0.97** | **3.50** |
| **p (pathogenic vs. VUS)*** | | | | | | **< 0.0001** | | **0.0005** | | **0.006** | | **< 0.0001** | | **0.07** | | **0.001** | | **0.009** | **0.05** | **0.03** | **0.02** |

VUS, variant of uncertain significance. Genomic co-ordinates are based on GRCh37/hg19 human reference sequence. Max.Freq., maximum reported minor allele frequency in 1000 genomes (phase 2 release) and the NHLBI exome sequencing project data sets. NA, novel variant. s.d., standard deviation.

*p value shows statistical significance at 5% level (two-tailed Mann-Whitney test)

In silico prediction scores are based on ANNOVAR version 2013aug23, full details available at: http://www.openbioinformatics.org/annovar/ and refer to the following specific ANNOVAR annotations: Polyphen: "LJB23_Polyphen2_HVAR_score", Mutation Taster: "LJB23_MutationTaster_score_converted", Mutation Assessor: "LJB23_MutationAssessor_score_converted", LRT: "LJB23_LRT_score_converted", FATHMM: "LJB23_FATHMM_score_converted"

**Predictive functional scores**

*SIFT, Polyphen, MutationTaster, MutationAssessor, LRT, FATHMM* : all scores converted to 0-1 scale, higher number = higher probability of functional significance

Cadd: shown as [raw score, scaled score]. Raw score: higher number = higher likelihood of deleterious variant. Scaled score: phred-like c-score (-10*log10(rank/total)) of variant pathogenicity ranked relative to all possible substitutions of the human genome such that, a scaled score >10 relates to the top 10% of variants ranked for pathogenicity, scaled score of >20 relates to the top 1% of ranked variants.

**Qualitative predictions**

D, deleterious. T, tolerated; [*Mutation Taster* only: A, disease causing automatic, D, disease causing; N, polymorphism; P, polymorphism automatic]

*[Mutation Assessor* only: H(high), M(medium and L(low) probability of functional impact]

**Table S9** Summary of genotype-phenotype correlation in Collagen genes in the EDS cohort

| Gene | Initial Clinical Diagnosis [a] | | | | | Mean Beighton score | Vascular complication [b] | Collagen [c] abnormality | LM/EM [c] abnormality |
|---|---|---|---|---|---|---|---|---|---|
| | Classical | Vascular | HM | Other EDS | Other HDCT | | | | |
| **Pathogenic variants** | | | | | | | | | |
| *COL1A1 / COL1A2* | | | | | 3 [d] | 5.5 | 0/3 | 1/1 | 1/1 |
| *COL3A1* | 2 | 11 | | | | 7.3 | 5/13 | 6/7 | 5/7 |
| *COL5A1 / COL5A2* | 7 | 1 | 1 | | | 6.3 | 1/9 | 2/3 | 4/5 |
| **VUS** | | | | | | | | | |
| *COL1A1 / COL1A2* | | 2 | 6 | | 2 | 5.7 | 3/10 | 1/5 [e] | 2/9 [e, f] |
| *COL3A1* | 1 | | 3 | | 1 | 6.0 | 2/5 | 0/2 | 2/3 [f] |
| *COL5A1 / COL5A2* | 1 | | 6 | | | 6.0 | 2/7 | 0/2 | 1/3 [f] |

EDS, Ehlers-Danlos syndrome. VUS, variant of uncertain clinical significance; No., number of patients with rare variant in corresponding gene; HDCT, Hereditary disorder of connective tissue; LM, light microscopy; EM, electron microscopy.

**a.** Initial Clinical Diagnosis refers to most applicable classification at first specialist EDS consultation: numbers shows the presenting clinical diagnoses for variants in each group. **b.** Vascular complication: one or more of the following clinical features at presentation: aortic or peripheral arterial aneurysm, dissection or rupture, cerebral aneurysm / subarachnoid haemorrhage, not including atherosclerotic vascular disease (incidence in mutation negative cases = 31.0%). **c.** numerator: no. patients with abnormality / denominator: number tested for abnormality. **d.** All 3 patients had features of osteogenesis imperfecta (Sillence criteria). **e.** One of these patients (ID 629) had some phenotypic features of EDS/OI overlap, broadening of the pro-α2(I) band (Collagen I) on SDS-PAGE and possible subtle collagen depletion on LM, but incomplete segregation of phenotype in 7 first-degree relatives tested. **f.** These represent two patients with more than one co-existing rare VUS (Patient ID 38 in *COL3A1* & *COL5A1*; Patient ID 39 in *COL3A1*, *COL1A2*; also *TNXB* gene duplication).